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(1) GENERAL INFORMATION:

(i) APPLICANT(S): Bradford C. Van Wagenen
 Manuel F. Balandrin
 Eric G. Del Mar
 Edward F. Nemeth

(ii) TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
MOLECULES

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Lyon & Lyon
(B) STREET: First Interstate World Center
Suite 4700
633 West Fifth Street
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 90071

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: FASTSEQ

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/484,159
(B) FILING DATE: 7 June, 1995
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

Prior applications total,
including application
described below: 9

(A) APPLICATION NUMBER: 08/353,784
(B) FILING DATE: 9 December, 1994

(viii) ATTORNEY/AGENT INFORMATION:

(ix) TELECOMMUNICATION INFORMATION:

(2) INFORMATION FOR SEQ ID NO: 1:

(A) LENGTH: 5275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 515..3769
 (C) OTHER INFORMATION:

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGGAAAAAAA	AAAAAAGTTC	CCCACTCTAG	TACAGAGAAG	GTTGGCAGAG	TCGTAAGCCC	60
CCAACCTCTT	AAACTTCTCT	GCATCTCCAA	GGAGAAGGAG	GGAAGAGGGG	TTCTTTCCGA	120
CCTGAGGAGC	TGGATCTGGG	GTCCGAGAAC	CCCAAGGTAG	CACCGGAAAG	AACAGCACAG	180
GAGGCGAGAG	CGTGGCCGGT	GGCCGGGAGA	ACCAGACCCG	ACGCGCGGTC	CTCGGCGCCG	240
GGGTCCCGGG	GACTCAGCTC	AGCACGACTG	GGAAGCCGAA	AGTACTACAC	ACGGTCTCTG	300
CATGATGTGA	CTTCTGAAGA	CTCAAGAGCC	ACCCAATTCA	CTAGTCTGCA	ATGGAGAAGG	360
CAGAAATGGA	AAGTCAAACC	CCACGGTTCC	ATTCTATTAA	TTCTGTAGAC	ATGTGCCCCC	420
ACTGCAGGGA	GTGAGTCGCA	CCAAGGGGGA	AAGTCCTCAG	GGGCCCCCAG	ACCACCAGCG	480
CTTGAGTCCC	TCTTCCTGGA	GAGAAAGCAG	AACT ATG GCA CTT TAT AGC TGC			532
			Met Ala Leu Tyr Ser Cys			
			1		5	
TGT TGG ATC	CTC TTG GCT	TTT TCT ACC	TGG TGC ACT	TCC GCC TAT	GGG	580
Cys Trp Ile	Leu Leu Ala	Phe Ser Thr	Trp Cys Thr	Ser Ala Tyr	Gly	
	10		15		20	
CCT GAC CAG	CGA GCC CAA	AAG AAA GGG	GAC ATT ATC	CTC GGG GGG	CTC	628
Pro Asp Gln	Arg Ala Gln	Lys Lys Gly	Asp Ile Ile	Leu Gly Gly	Leu	
	25		30		35	
TTT CCT ATT	CAT TTT GGG	GTT GCA GTG	AAA GAT CAG	GAT CTA AAG	TCG	676
Phe Pro Ile	His Phe Gly	Val Ala Val	Lys Asp Gln	Asp Leu Lys	Ser	
	40		45		50	
AGG CCG GAG	TCC GTG GAG	TGT ATC AGG	TAT AAT TTC	CGA GGA TTT	CGC	724
Arg Pro Glu	Ser Val Glu	Cys Ile Arg	Tyr Asn Phe	Arg Gly Phe	Arg	
	55		60		65	70
TGG TTA CAA	GCT ATG ATA	TTT GCC ATA	GAG GAA ATA	AAC AGC AGT	CCA	772
Trp Leu Gln	Ala Met Ile	Phe Ala Ile	Glu Glu Ile	Asn Ser Ser	Pro	
	75		80		85	
GCC CTT CTT	CCC AAC ATG	ACC CTG GGA	TAC AGG ATA	TTC GAC ACT	TGT	820
Ala Leu Leu	Pro Asn Met	Thr Leu Gly	Tyr Arg Ile	Phe Asp Thr	Cys	
	90		95		100	
AAC ACC GTC	TCT AAA GCC	TTG GAG GCC	ACC CTG AGT	TTT GTG GCC	CAG	868
Asn Thr Val	Ser Lys Ala	Leu Glu Ala	Thr Leu Ser	Phe Val Ala	Gln	
	105		110		115	

CGGAAAAAAA

AAC Asn	AAA Lys	ATT Ile	GAC Asp	TCT Ser	TTG Leu	AAC Asn	CTT Leu	GAT Asp	GAG Glu	TTC Phe	TGC Cys	AAC Asn	TGC Cys	TCA Ser	GAG Glu	916
120 125 130																
CAC His	ATC Ile	CCC Pro	TCT Ser	ACC Thr	ATC Ile	GCA Ala	GTG Val	GTG Val	GGA Gly	GCT Ala	ACT Thr	GGC Gly	TCG Ser	GGC Gly	ATC Ile	964
135 140 145 150																
TCC Ser	ACA Thr	GCA Ala	GTG Val	GCC Ala	AAC Asn	CTG Leu	CTG Leu	GGG Gly	CTC Leu	TTC Phe	TAC Tyr	ATC Ile	CCC Pro	CAG Gln	GTC Val	1012
155 160 165																
AGC Ser	TAT Tyr	GCC Ala	TCC Ser	TCC Ser	AGC Ser	AGA Arg	CTC Leu	CTC Leu	AGC Ser	AAC Asn	AAG Lys	AAT Asn	CAA Gln	TTC Phe	AAG Lys	1060
170 175 180																
TCC Ser	TTC Phe	CTC Leu	CGC Arg	ACC Thr	ATA Ile	CCC Pro	AAT Asn	GAT Asp	GAA Glu	CAC His	CAG Gln	GCC Ala	ACG Thr	GCC Ala	ATG Met	1108
185 190 195																
GCT Ala	GAC Asp	ATC Ile	ATC Ile	GAG Glu	TAC Tyr	TTC Phe	CGC Arg	TGG Trp	AAC Asn	TGG Trp	GTG Val	GGC Gly	ACA Thr	ATT Ile	GCA Ala	1156
200 205 210																
GCT Ala	GAC Asp	GAT Asp	GAC Asp	TAT Tyr	GGC Gly	CGG Arg	CCA Pro	GGG Gly	ATC Ile	GAG Glu	AAG Lys	TTT Phe	CGA Arg	GAG Glu	GAA Glu	1204
215 220 225 230																
GCT Ala	GAG Glu	GAG Glu	AGG Arg	GAC Asp	ATC Ile	TGC Cys	ATC Ile	GAC Asp	TTC Phe	AGC Ser	GAG Glu	CTC Leu	ATC Ile	TCC Ser	CAA Gln	1252
235 240 245																
TAC Tyr	TCT Ser	GAT Asp	GAG Glu	GAA Glu	AAG Lys	ATC Ile	CAG Gln	CAG Gln	GTG Val	GTG Val	GAG Glu	GTG Val	ATC Ile	CAG Gln	AAT Asn	1300
250 255 260																
TCC Ser	ACC Thr	GCC Ala	AAA Lys	GTC Val	ATT Ile	GTC Val	GTC Val	TTC Phe	TCC Ser	AGC Ser	GGC Gly	CCA Pro	GAC Asp	CTG Leu	GAA Glu	1348
265 270 275																
CCC Pro	CTC Leu	ATC Ile	AAA Lys	GAG Glu	ATC Ile	GTC Val	CGG Arg	CGC Arg	AAT Asn	ATC Ile	ACA Thr	GGC Gly	AGG Arg	ATC Ile	TGG Trp	1396
280 285 290																
CTG Leu	GCC Ala	AGC Ser	GAG Glu	GCC Ala	TGG Trp	GCC Ala	AGC Ser	TCT Ser	TCC Ser	CTG Leu	ATT Ile	GCT Ala	ATG Met	CCC Pro	GAG Glu	1444
295 300 305 310																
TAT Tyr	TTC Phe	CAT His	GTG Val	GTC Val	GGA Gly	GGC Gly	ACC Thr	ATT Ile	GGG Gly	TTT Phe	GGT Gly	TTG Leu	AAA Lys	GCT Ala	GGG Gly	1492
315 320 325																
CAG Gln	ATC Ile	CCA Pro	GGC Gly	TTC Phe	CGG Arg	GAA Glu	TTC Phe	CTG Leu	CAG Gln	AAA Lys	GTC Val	CAC His	CCC Pro	AGG Arg	AAG Lys	1540
330 335 340																

TCT Ser	GTC Val	CAC His 345	AAT Asn	GGT Gly	TTT Phe	GCC Ala	AAG Lys 350	GAG Glu	TTT Phe	TGG Trp	GAA Glu	GAA Glu 355	ACA Thr	TTT Phe	AAC Asn	1588
TGC Cys	CAC His 360	CTG Leu	CAA Gln	GAG Glu	GGT Gly	GCT Ala 365	AAA Lys	GGC Gly	CCA Pro	TTA Leu	CCG Pro 370	GTG Val	GAC Asp	ACC Thr	TTC Phe	1636
CTG Leu 375	AGA Arg	GGT Gly	CAC His	GAA Glu 380	GAA Glu	GGA Gly	GGT Gly	GCC Ala	AGG Arg	TTA Leu 385	AGC Ser	AAC Asn	AGT Ser	CCC Pro	ACT Thr 390	1684
GCC Ala	TTC Phe	CGA Arg	CCT Pro	CTG Leu 395	TGC Cys	ACT Thr	GGG Gly	GAG Glu	GAG Glu 400	AAC Asn	ATC Ile	AGC Ser	AGT Ser	GTC Val 405	GAG Glu	1732
ACT Thr	CCT Pro	TAC Tyr	ATG Met 410	GAT Asp	TAT Tyr	ACA Thr	CAT His	TTA Leu 415	CGG Arg	ATA Ile	TCC Ser	TAC Tyr	AAC Asn 420	GTC Val	TAC Tyr	1780
TTA Leu	GCC Ala	GTC Val 425	TAC Tyr	TCC Ser	ATT Ile	GCT Ala	CAT His 430	GCC Ala	CTA Leu	CAA Gln	GAT Asp	ATA Ile 435	TAC Tyr	ACC Thr	TGC Cys	1828
ATA Ile	CCT Pro 440	GGG Gly	AGA Arg	GGG Gly	CTC Leu	TTC Phe 445	ACC Thr	AAC Asn	GGT Gly	TCC Ser	TGC Cys 450	GCA Ala	GAT Asp	ATC Ile	AAG Lys	1876
AAG Lys 455	GTT Val	GAA Glu	GCT Ala	TGG Trp	CAG Gln 460	GTC Val	CTG Leu	AAA Lys	CAC His	CTG Leu 465	CGG Arg	CAC His	CTA Leu	AAT Asn	TTT Phe 470	1924
ACC Thr	AGC Ser	AAT Asn	ATG Met	GGG Gly 475	GAG Glu	CAA Gln	GTA Val	ACT Thr	TTC Phe 480	GAT Asp	GAA Glu	TGT Cys	GGA Gly	GAC Asp 485	CTG Leu	1972
GCA Ala	GGG Gly	AAC Asn	TAT Tyr 490	TCC Ser	ATC Ile	ATC Ile	AAC Asn	TGG Trp 495	CAC His	CTC Leu	TCC Ser	CCA Pro	GAG Glu 500	GAC Asp	GGC Gly	2020
TCC Ser	ATA Ile	GTG Val 505	TTT Phe	AAG Lys	GAA Glu	GTT Val	GGA Gly 510	TAT Tyr	TAC Tyr	AAT Asn	GTC Val	TAT Tyr 515	GCC Ala	AAG Lys	AAA Lys	2068
GGA Gly	GAG Glu 520	AGA Arg	CTC Leu	TTC Phe	ATC Ile	AAT Asn 525	GAT Asp	GAA Glu	AAA Lys	ATT Ile	CTG Leu 530	TGG Trp	AGT Ser	GGA Gly	TTC Phe	2116
TCA Ser 535	AGG Arg	GAG Glu	GTG Val	CCT Pro	TTC Phe 540	TCC Ser	AAC Asn	TGC Cys	AGT Ser	CGA Arg 545	GAC Asp	TGC Cys	CTG Leu	GCA Ala	GGG Gly 550	2164
ACC Thr	AGG Arg	AAA Lys	GGA Gly	ATC Ile 555	ATT Ile	GAG Glu	GGG Gly	GAG Glu	CCC Pro 560	ACC Thr	TGC Cys	TGC Cys	TTT Phe 565	GAG Glu	TGT Cys	2212

GTG Val	GAA Glu	TGT Cys	CCT Pro 570	GAT Asp	GGG Gly	GAG Glu	TAC Tyr	AGC Ser 575	GAC Asp	GAG Glu	ACA Thr	GAT Asp 580	GCA Ala	AGT Ser	GCC Ala	2260
TGT Cys	GAT Asp 585	AAG Lys	TGC Cys	CCT Pro	GAT Asp	GAC Asp	TTC Phe 590	TGG Trp	TCC Ser	AAT Asn	GAG Glu	AAC Asn 595	CAC His	ACT Thr	TCC Ser	2308
TGC Cys 600	ATC Ile	GCC Ala	AAG Lys	GAG Glu	ATC Ile	GAG Glu 605	TTT Phe	CTG Leu	TCG Ser	TGG Trp	ACC Thr 610	GAG Glu	CCC Pro	TTC Phe	GGG Gly	2356
ATC Ile 615	GCA Ala	CTC Leu	ACG Thr	CTC Leu	TTT Phe 620	GCT Ala	GTG Val	CTG Leu	GGC Gly	ATT Ile 625	TTC Phe	CTC Leu	ACA Thr	GCC Ala	TTC Phe 630	2404
GTG Val	CTG Leu	GGC Gly	GTC Val 635	TTC Phe	ATC Ile	AAG Lys	TTC Phe	CGC Arg 640	AAC Asn	ACG Thr	CCC Pro	ATC Ile	GTC Val	AAG Lys 645	GCC Ala	2452
ACC Thr	AAC Asn	CGG Arg 650	GAG Glu	CTC Leu	TCC Ser	TAT Tyr	CTC Leu	CTT Leu 655	CTC Leu	TTC Phe	TCC Ser	CTG Leu 660	CTC Leu	TGC Cys	TGC Cys	2500
TTC Phe	TCC Ser 665	AGC Ser	TCC Ser	CTG Leu	TTC Phe	TTC Phe	ATC Ile 670	GGG Gly	GAG Glu	CCC Pro	CAG Gln 675	GAC Asp	TGG Trp	ACG Thr	TGC Cys	2548
CGC Arg 680	CTG Leu	CGC Arg	CAG Gln	CCG Pro	GCC Ala	TTT Phe 685	GGC Gly	ATC Ile	AGC Ser	TTC Phe	GTG Val 690	CTC Leu	TGC Cys	ATC Ile	TCG Ser	2596
TGC Cys 695	ATC Ile	CTG Leu	GTG Val	AAA Lys 700	ACC Thr	AAT Asn	CGG Arg	GTC Val	CTC Leu	CTG Leu 705	GTG Val	TTT Phe	GAG Glu	GCC Ala	AAG Lys 710	2644
ATT Ile	CCC Pro	ACC Thr	AGC Ser 715	TTC Phe	CAC His	CGG Arg	AAG Lys	TGG Trp 720	TGG Trp	GGG Gly	CTC Leu	AAC Asn	CTG Leu 725	CAG Gln	TTC Phe	2692
CTG Leu	CTG Leu	GTC Val	TTC Phe 730	CTC Leu	TGC Cys	ACC Thr	TTC Phe	ATG Met 735	CAG Gln	ATT Ile	GTC Val	ATC Ile	TGT Cys 740	GCC Ala	ATT Ile	2740
TGG Trp	CTC Leu	AAT Asn 745	ACA Thr	GCG Ala	CCC Pro	CCC Pro	TCG Ser 750	AGC Ser	TAC Tyr	CGC Arg	AAC Asn 755	CAC His	GAG Glu	CTG Leu	GAG Glu	2788
GAC Asp 760	GAG Glu	ATC Ile	ATC Ile	TTC Phe	ATC Ile	ACC Thr 765	TGC Cys	CAC His	GAG Glu	GGC Gly	TCG Ser 770	CTC Leu	ATG Met	GCG Ala	CTG Leu	2836
GGC Gly 775	TTC Phe	CTG Leu	ATC Ile	GGC Gly	TAC Tyr 780	ACC Thr	TGC Cys	TTG Leu	CTG Leu	GCC Ala 785	GCC Ala	ATC Ile	TGC Cys	TTC Phe	TTC Phe 790	2884

TTC	GCC	TTC	AAG	TCC	CGG	AAG	CTG	CCA	GAG	AAC	TTC	AAT	GAA	GCC	AAG	2932
Phe	Ala	Phe	Lys	Ser	Arg	Lys	Leu	Pro	Glu	Asn	Phe	Asn	Glu	Ala	Lys	
				795					800					805		
TTC	ATC	ACC	TTC	AGC	ATG	CTC	ATC	TTC	TTC	ATC	GTC	TGG	ATC	TCT	TTC	2980
Phe	Ile	Thr	Phe	Ser	Met	Leu	Ile	Phe	Phe	Ile	Val	Trp	Ile	Ser	Phe	
			810					815					820			
ATC	CCC	GCC	TAC	GCC	AGC	ACT	TAC	GGC	AAG	TTC	GTC	TCT	GCC	GTG	GAG	3028
Ile	Pro	Ala	Tyr	Ala	Ser	Thr	Tyr	Gly	Lys	Phe	Val	Ser	Ala	Val	Glu	
		825					830					835				
GTG	ATC	GCC	ATC	CTG	GCG	GCC	AGC	TTT	GGC	TTG	CTG	GCC	TGT	ATC	TTC	3076
Val	Ile	Ala	Ile	Leu	Ala	Ala	Ser	Phe	Gly	Leu	Leu	Ala	Cys	Ile	Phe	
	840					845					850					
TTC	AAC	AAG	GTC	TAC	ATC	ATC	CTC	TTC	AAG	CCT	TCC	CGG	AAC	ACC	ATC	3124
Phe	Asn	Lys	Val	Tyr	Ile	Ile	Leu	Phe	Lys	Pro	Ser	Arg	Asn	Thr	Ile	
855					860					865					870	
GAG	GAG	GTG	CGC	TGC	AGC	ACC	GCG	GCA	CAC	GCC	TTC	AAG	GTG	GCC	GCC	3172
Glu	Glu	Val	Arg	Cys	Ser	Thr	Ala	Ala	His	Ala	Phe	Lys	Val	Ala	Ala	
				875					880					885		
CGA	GCC	ACG	CTG	CGC	CGC	AGC	AAC	GTC	TCC	CGC	CAG	CGG	TCC	AGC	AGC	3220
Arg	Ala	Thr	Leu	Arg	Arg	Ser	Asn	Val	Ser	Arg	Gln	Arg	Ser	Ser	Ser	
			890					895					900			
CTA	GGG	GGC	TCC	ACG	GGA	TCC	ACC	CCC	TCC	TCC	TCC	ATC	AGC	AGC	AAG	3268
Leu	Gly	Gly	Ser	Thr	Gly	Ser	Thr	Pro	Ser	Ser	Ser	Ile	Ser	Ser	Lys	
		905					910					915				
AGC	AAC	AGC	GAG	GAC	CCG	TTC	CCT	CAG	CAG	CAG	CCG	AAG	AGG	CAG	AAG	3316
Ser	Asn	Ser	Glu	Asp	Pro	Phe	Pro	Gln	Gln	Gln	Pro	Lys	Arg	Gln	Lys	
	920					925					930					
CAG	CCG	CAG	CCG	CTG	GCC	CTG	AGC	CCG	CAC	AAC	GCG	CAG	CAG	CCA	CAG	3364
Gln	Pro	Gln	Pro	Leu	Ala	Leu	Ser	Pro	His	Asn	Ala	Gln	Gln	Pro	Gln	
935					940					945					950	
CCG	CGG	CCA	CCC	TCG	ACC	CCA	CAG	CCG	CAG	CCA	CAG	TCG	CAG	CAG	CCG	3412
Pro	Arg	Pro	Pro	Ser	Thr	Pro	Gln	Pro	Gln	Pro	Gln	Ser	Gln	Gln	Pro	
				955					960					965		
CCC	CGA	TGC	AAG	CAG	AAG	GTC	ATC	TTC	GGC	AGC	GGC	ACC	GTC	ACC	TTC	3460
Pro	Arg	Cys	Lys	Gln	Lys	Val	Ile	Phe	Gly	Ser	Gly	Thr	Val	Thr	Phe	
			970					975					980			
TCG	CTG	AGC	TTT	GAC	GAG	CCT	CAG	AAG	ACC	GCC	GTG	GCT	CAC	AGG	AAT	3508
Ser	Leu	Ser	Phe	Asp	Glu	Pro	Gln	Lys	Thr	Ala	Val	Ala	His	Arg	Asn	
		985					990					995				
TCC	ACG	CAC														

ACC AAA CAC CAG GCG TTG CTC CCG CTG CAG TGC GGA GAG ACG GAC TCA	3604
Thr Lys His Gln Ala Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp Ser	
1015 1020 1025 1030	
GAA TTG ACC TCC CAG GAG ACA GGC CTG CAG GGC CCT GTG GGT GAG GAC	3652
Glu Leu Thr Ser Gln Glu Thr Gly Leu Gln Gly Pro Val Gly Glu Asp	
1035 1040 1045	
CAC CAG CTA GAG ATG GAG GAC CCC GAA GAG ATG TCC CCG GCA CTT GTA	3700
His Gln Leu Glu Met Glu Asp Pro Glu Glu Met Ser Pro Ala Leu Val	
1050 1055 1060	
GTG TCT AAT TCC CGG AGC TTT GTC ATC AGT GGC GGA GGC AGC ACT GTT	3748
Val Ser Asn Ser Arg Ser Phe Val Ile Ser Gly Gly Gly Ser Thr Val	
1065 1070 1075	
ACG GAA AAC ATG CTG CGT TCT TAAAAGGGAA GGAGAAAGCC AGTTCAGGGG	3799
Thr Glu Asn Met Leu Arg Ser	
1080 1085	
GAATCCAGGC AGTTTCCCCG GGATGACCTT CTCCAAAGGG ATGAGGAACT GGGGGGGCAC	3859
CCCCACCCCC TTCCTCCAGG AAGGAGGGAT AAGACCCACC AAATGCTTGG AACTTAGTTG	3919
CACTGCTATA AACGACAGTG AATGAAATAA TGTCCCCCTT AAAATTAAAA AGAGGGGAGC	3979
GGTGTGCTTC TGTGGTTAGG TTTATCAGAG TGCTGAGATC CCTATAGTCA GGTTCGCCTT	4039
TCCTATCCCT GCTTCCATTC TCCTCTTCTG TTCTATCCCA TCCAACAGTC CAGAGATAAA	4099
ACCATGGCTT TAAGATACCC ACCTATTCCC CCTAGGGTCT TATTTGTTGT TTTTGTGCT	4159
GTTGTTTTGG TTTGATTTTT GTTTTTAATG TTGAAACGTC TGCCCTGAAC TTTGCAGACA	4219
GCCTGGTCCA AAAACAAACC TGTGCAGAGT GACAGGACCT CCTATGGGCA CCACTAGAGT	4279
TGAGTGCGAA AGACAGAATG TCGCCAGCGC TGCCCAACAC CTTGACAGTG GGAAGAACTT	4339
GAAATGTCCA GAGCTGTAAG ATGAATGTGT CCCCTCCTAT TTATGAAAAA TGTTAAATAT	4399
GTGGTTTCCT ACTTGCTGCT GCTGTCACGT GACATGGAGA AGGTTAGCAT CCATCCTCCA	4459
GCAGTATGTC TGATCTTGTC CAGAGTGTGA TGGTGATGCC ACGTTTAGAT TCCAATATCT	4519
CAGGAATCAC CTCAGCCTGC ATGAATCCAA TGAGCTGTAT CTGTAATTAA TATTGTCATA	4579
TGTAGCTTTA TCCTTAAGAA AATGTGTTTG TTTTAATAGT CCGTGGAAAA TATAAGCTGG	4639
AAAAAATGTC CCAGTCTGGT TGATATAAGG CAGTATTATT GAGTCCCGTT TTCTTTGCCC	4699
GCCCCACCAC CCACACCCCA ATGAGCTAAG CCCTAAATGA GCCCTTTCAG GGGCCAGGGA	4759
TCCAGAAGCT CCCTCTTTCT CCACCCCAAA CGCTTCCTGA AGTCAGATCC ATGCCTTTCC	4819
CTGTGAAGAA TAAGCTCCCA GTCTCTGACC TCCTACCAGT TTCTGGGGTA AGAACACGTG	4879

5275

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: cDNA to mRNA

(A) NAME/KEY: CDS
(B) LOCATION: 436..3699
(D) OTHER INFORMATION:

GCTGCTGTGG	CCGGACCCGA	AGGCGGGCGC	CGGGAGCGCA	GCGAGCCAGA	CGCGCCTCTC	60
CAAGACCGTG	ACCTTGGCAT	AGGGAGCGGG	GCTGCGCGCA	GTCCTGAGAT	CAGACCAGAG	120
CTCATCCTCG	TGGAGACCCA	CGGCCGAGGG	GCCGGAGCTG	CCTCTGTGCG	AGGGAGCCCT	180
GGCCGCGGCG	CAGAAGGCAT	CACAGGAGGC	CTCTGCATGA	TGTGGCTTCC	AAAGACTCAA	240
GGACCACCCA	CATTACAAGT	CTGGATTGAG	GAAGGCAGAA	ATGGAGATTC	AAACACCACG	300
TCTTCTATTA	TTTTATTAAT	CAATCTGTAG	ACATGTGTCC	CCACTGCAGG	GAGTGAAGTG	360
CTCCAAGGGA	GAAACTTCTG	GGAGCCTCCA	AACTCCTAGC	TGTCTCATCC	CTTGCCCTGG	420

AGAGACGGCA	GAACC	ATG	GCA	TTT	TAT	AGC	TGC	TGC	TGG	GTC	CTC	TTG	GCA	471		
		Met	Ala	Phe	Tyr	Ser	Cys	Cys	Trp	Val	Leu	Leu	Ala			
		1				5					10					
CTC	ACC	TGG	CAC	ACC	TCT	GCC	TAC	GGG	CCA	GAC	CAG	CGA	GCC	CAA	AAG	519
Leu	Thr	Trp	His	Thr	Ser	Ala	Tyr	Gly	Pro	Asp	Gln	Arg	Ala	Gln	Lys	
		15					20				25					
AAG	GGG	GAC	ATT	ATC	CTT	GGG	GGG	CTC	TTT	CCT	ATT	CAT	TTT	GGA	GTA	567
Lys	Gly	Asp	Ile	Ile	Leu	Gly	Gly	Leu	Phe	Pro	Ile	His	Phe	Gly	Val	
	30					35					40					
GCA	GCT	AAA	GAT	CAA	GAT	CTC	AAA	TCA	AGG	CCG	GAG	TCT	GTG	GAA	TGT	615
Ala	Ala	Lys	Asp	Gln	Asp	Leu	Lys	Ser	Arg	Pro	Glu	Ser	Val	Glu	Cys	
45					50					55					60	
ATC	AGG	TAT	AAT	TTC	CGT	GGG	TTT	CGC	TGG	TTA	CAG	GCT	ATG	ATA	TTT	663
Ile	Arg	Tyr	Asn	Phe	Arg	Gly	Phe	Arg	Trp	Leu	Gln	Ala	Met	Ile	Phe	
				65					70					75		
GCC	ATA	GAG	GAG	ATA	AAC	AGC	AGC	CCA	GCC	CTT	CTT	CCC	AAC	TTG	ACG	711
Ala	Ile	Glu	Glu	Ile	Asn	Ser	Ser	Pro	Ala	Leu	Leu	Pro	Asn	Leu	Thr	
				80				85					90			
CTG	GGA	TAC	AGG	ATA	TTT	GAC	ACT	TGC	AAC	ACC	GTT	TCT	AAG	GCC	TTG	759
Leu	Gly	Tyr	Arg	Ile	Phe	Asp	Thr	Cys	Asn	Thr	Val	Ser	Lys	Ala	Leu	
		95					100					105				
GAA	GCC	ACC	CTG	AGT	TTT	GTT	GCT	CAA	AAC	AAA	ATT	GAT	TCT	TTG	AAC	807
Glu	Ala	Thr	Leu	Ser	Phe	Val	Ala	Gln	Asn	Lys	Ile	Asp	Ser	Leu	Asn	
	110					115					120					
CTT	GAT	GAG	TTC	TGC	AAC	TGC	TCA	GAG	CAC	ATT	CCC	TCT	ACG	ATT	GCT	855
Leu	Asp	Glu	Phe	Cys	Asn	Cys	Ser	Glu	His	Ile	Pro	Ser	Thr	Ile	Ala	
125					130					135					140	
GTG	GTG	GGA	GCA	ACT	GGC	TCA	GGC	GTC	TCC	ACG	GCA	GTG	GCA	AAT	CTG	903
Val	Val	Gly	Ala	Thr	Gly	Ser	Gly	Val	Ser	Thr	Ala	Val	Ala	Asn	Leu	
				145					150					155		
CTG	GGG	CTC	TTC	TAC	ATT	CCC	CAG	GTC	AGT	TAT	GCC	TCC	TCC	AGC	AGA	951
Leu	Gly	Leu	Phe	Tyr	Ile	Pro	Gln	Val	Ser	Tyr	Ala	Ser	Ser	Ser	Arg	
			160					165					170			
CTC	CTC	AGC	AAC	AAG	AAT	CAA	TTC	AAG	TCT	TTC	CTC	CGA	ACC	ATC	CCC	999
Leu	Leu	Ser	Asn	Lys	Asn	Gln	Phe	Lys	Ser	Phe	Leu	Arg	Thr	Ile	Pro	
		175					180					185				
AAT	GAT	GAG	CAC	CAG	GCC	ACT	GCC	ATG	GCA	GAC	ATC	ATC	GAG	TAT	TTC	1047
Asn	Asp	Glu	His	Gln	Ala	Thr	Ala	Met	Ala	Asp	Ile	Ile	Glu	Tyr	Phe	
	190					195					200					
CGC	TGG	AAC	TGG	GTG	GGC	ACA	ATT	GCA	GCT	GAT	GAC	GAC	TAT	GGG	CGG	1095
Arg	Trp	Asn	Trp	Val	Gly	Thr	Ile	Ala	Ala	Asp	Asp	Asp	Tyr	Gly	Arg	
205					210					215					220	

CCG	GGG	ATT	GAG	AAA	TTC	CGA	GAG	GAA	GCT	GAG	GAA	AGG	GAT	ATC	TGC	1143
Pro	Gly	Ile	Glu	Lys	Phe	Arg	Glu	Glu	Ala	Glu	Glu	Arg	Asp	Ile	Cys	
				225					230					235		
ATC	GAC	TTC	AGT	GAA	CTC	ATC	TCC	CAG	TAC	TCT	GAT	GAG	GAA	GAG	ATC	1191
Ile	Asp	Phe	Ser	Glu	Leu	Ile	Ser	Gln	Tyr	Ser	Asp	Glu	Glu	Glu	Ile	
			240					245					250			
CAG	CAT	GTG	GTA	GAG	GTG	ATT	CAA	AAT	TCC	ACG	GCC	AAA	GTC	ATC	GTG	1239
Gln	His	Val	Val	Glu	Val	Ile	Gln	Asn	Ser	Thr	Ala	Lys	Val	Ile	Val	
		255					260					265				
GTT	TTC	TCC	AGT	GGC	CCA	GAT	CTT	GAG	CCC	CTC	ATC	AAG	GAG	ATT	GTC	1287
Val	Phe	Ser	Ser	Gly	Pro	Asp	Leu	Glu	Pro	Leu	Ile	Lys	Glu	Ile	Val	
	270					275					280					
CGG	CGC	AAT	ATC	ACG	GGC	AAG	ATC	TGG	CTG	GCC	AGC	GAG	GCC	TGG	GCC	1335
Arg	Arg	Asn	Ile	Thr	Gly	Lys	Ile	Trp	Leu	Ala	Ser	Glu	Ala	Trp	Ala	
285					290					295					300	
AGC	TCC	TCC	CTG	ATC	GCC	ATG	CCT	CAG	TAC	TTC	CAC	GTG	GTT	GGC	GGC	1383
Ser	Ser	Ser	Leu	Ile	Ala	Met	Pro	Gln	Tyr	Phe	His	Val	Val	Gly	Gly	
			305					310						315		
ACC	ATT	GGA	TTC	GCT	CTG	AAG	GCT	GGG	CAG	ATC	CCA	GGC	TTC	CGG	GAA	1431
Thr	Ile	Gly	Phe	Ala	Leu	Lys	Ala	Gly	Gln	Ile	Pro	Gly	Phe	Arg	Glu	
			320					325					330			
TTC	CTG	AAG	AAG	GTC	CAT	CCC	AGG	AAG	TCT	GTC	CAC	AAT	GGT	TTT	GCC	1479
Phe	Leu	Lys	Lys	Val	His	Pro	Arg	Lys	Ser	Val	His	Asn	Gly	Phe	Ala	
		335					340					345				
AAG	GAG	TTT	TGG	GAA	GAA	ACA	TTT	AAC	TGC	CAC	CTC	CAA	GAA	GGT	GCA	1527
Lys	Glu	Phe	Trp	Glu	Glu	Thr	Phe	Asn	Cys	His	Leu	Gln	Glu	Gly	Ala	
	350					355					360					
AAA	GGA	CCT	TTA	CCT	GTG	GAC	ACC	TTT	CTG	AGA	GGT	CAC	GAA	GAA	AGT	1575
Lys	Gly	Pro	Leu	Pro	Val	Asp	Thr	Phe	Leu	Arg	Gly	His	Glu	Glu	Ser	
365					370					375					380	
GGC	GAC	AGG	TTT	AGC	AAC	AGC	TCG	ACA	GCC	TTC	CGA	CCC	CTC	TGT	ACA	1623
Gly	Asp	Arg	Phe	Ser	Asn	Ser	Ser	Thr	Ala	Phe	Arg	Pro	Leu	Cys	Thr	
				385					390					395		
GGG	GAT	GAG	AAC	ATC	AGC	AGT	GTC	GAG	ACC	CCT	TAC	ATA	GAT	TAC	ACG	1671
Gly	Asp	Glu	Asn	Ile	Ser	Ser	Val	Glu	Thr	Pro	Tyr	Ile	Asp	Tyr	Thr	
			400					405					410			
CAT	TTA	CGG	ATA	TCC	TAC	AAT	GTG	TAC	TTA	GCA	GTC	TAC	TCC	ATT	GCC	1719
His	Leu	Arg	Ile	Ser	Tyr	Asn	Val	Tyr	Leu	Ala	Val	Tyr	Ser	Ile	Ala	
		415					420					425				
CAC	GCC	TTG	CAA	GAT	ATA	TAT	ACC	TGC	TTA	CCT	GGG	AGA	GGG	CTC	TTC	1767
His	Ala	Leu	Gln	Asp	Ile	Tyr	Thr	Cys	Leu	Pro	Gly	Arg	Gly	Leu	Phe	
	430					435					440					

ACC Thr 445	AAT Asn	GGC Gly	TCC Ser	TGT Cys	GCA Ala 450	GAC Asp	ATC Ile	AAG Lys	AAA Lys	GTT Val 455	GAG Glu	GCG Ala	TGG Trp	CAG Gln 460	GTC Val	1815
CTG Leu	AAG Lys	CAC His	CTA Leu	CGG Arg 465	CAT His	CTA Leu	AAC Asn	TTT Phe	ACA Thr 470	AAC Asn	AAT Asn	ATG Met	GGG Gly	GAG Glu 475	CAG Gln	1863
GTG Val	ACC Thr	TTT Phe	GAT Asp 480	GAG Glu	TGT Cys	GGT Gly	GAC Asp	CTG Leu 485	GTG Val	GGG Gly	AAC Asn	TAT Tyr	TCC Ser 490	ATC Ile	ATC Ile	1911
AAC Asn	TGG Trp	CAC His 495	CTC Leu	TCC Ser	CCA Pro	GAG Glu	GAT Asp 500	GGC Gly	TCC Ser	ATC Ile	GTG Val	TTT Phe 505	AAG Lys	GAA Glu	GTC Val	1959
GGG Gly 510	TAT Tyr	TAC Tyr	AAC Asn	GTC Val	TAT Tyr	GCC Ala 515	AAG Lys	AAG Lys	GGA Gly	GAA Glu	AGA Arg 520	CTC Leu	TTC Phe	ATC Ile	AAC Asn	2007
GAG Glu 525	GAG Glu	AAA Lys	ATC Ile	CTG Leu	TGG Trp 530	AGT Ser	GGG Gly	TTC Phe	TCC Ser	AGG Arg 535	GAG Glu	CCA Pro	CTC Leu	ACC Thr	TTT Phe 540	2055
GTG Val	CTG Leu	TCT Ser	GTC Val	CTC Leu 545	CAG Gln	GTG Val	CCC Pro	TTC Phe	TCC Ser 550	AAC Asn	TGC Cys	AGC Ser	CGA Arg	GAC Asp 555	TGC Cys	2103
CTG Leu	GCA Ala	GGG Gly	ACC Thr 560	AGG Arg	AAA Lys	GGG Gly	ATC Ile	ATT Ile 565	GAG Glu	GGG Gly	GAG Glu	CCC Pro	ACC Thr 570	TGC Cys	TGC Cys	2151
TTT Phe	GAG Glu	TGT Cys 575	GTG Val	GAG Glu	TGT Cys	CCT Pro	GAT Asp 580	GGG Gly	GAG Glu	TAT Tyr	AGT Ser	GAT Asp 585	GAG Glu	ACA Thr	GAT Asp	2199
GCC Ala 590	AGT Ser	GCC Ala	TGT Cys	AAC Asn	AAG Lys	TGC Cys 595	CCA Pro	GAT Asp	GAC Asp	TTC Phe	TGG Trp 600	TCC Ser	AAT Asn	GAG Glu	AAC Asn	2247
CAC His 605	ACC Thr	TCC Ser	TGC Cys	ATT Ile	GCC Ala 610	AAG Lys	GAG Glu	ATC Ile	GAG Glu	TTT Phe 615	CTG Leu	TCG Ser	TGG Trp	ACG Thr	GAG Glu 620	2295
CCC Pro	TTT Phe	GGG Gly	ATC Ile	GCA Ala 625	CTC Leu	ACC Thr	CTC Leu	TTT Phe	GCC Ala 630	GTG Val	CTG Leu	GGC Gly	ATT Ile	TTC Phe 635	CTG Leu	2343
ACA Thr	GCC Ala	TTT Phe	GTG Val 640	CTG Leu	GGT Gly	GTG Val	TTT Phe	ATC Ile 645	AAG Lys	TTC Phe	CGC Arg	AAC Asn	ACA Thr 650	CCC Pro	ATT Ile	2391
GTC Val	AAG Lys	GCC Ala 655	ACC Thr	AAC Asn	CGA Arg	GAG Glu	CTC Leu 660	TCC Ser	TAC Tyr	CTC Leu	CTC Leu	CTC Leu 665	TTC Phe	TCC Ser	CTG Leu	2439

CTC	TGC	TGC	TTC	TCC	AGC	TCC	CTG	TTC	TTC	ATC	GGG	GAG	CCC	CAG	GAC	2487
Leu	Cys	Cys	Phe	Ser	Ser	Ser	Leu	Phe	Phe	Ile	Gly	Glu	Pro	Gln	Asp	
670						675					680					
TGG	ACG	TGC	CGC	CTG	CGC	CAG	CCG	GCC	TTT	GGC	ATC	AGC	TTC	GTG	CTC	2535
Trp	Thr	Cys	Arg	Leu	Arg	Gln	Pro	Ala	Phe	Gly	Ile	Ser	Phe	Val	Leu	
685					690					695					700	
TGC	ATC	TCA	TGC	ATC	CTG	GTG	AAA	ACC	AAC	CGT	GTC	CTC	CTG	GTG	TTT	2583
Cys	Ile	Ser	Cys	Ile	Leu	Val	Lys	Thr	Asn	Arg	Val	Leu	Leu	Val	Phe	
				705					710					715		
GAG	GCC	AAG	ATC	CCC	ACC	AGC	TTC	CAC	CGC	AAG	TGG	TGG	GGG	CTC	AAC	2631
Glu	Ala	Lys	Ile	Pro	Thr	Ser	Phe	His	Arg	Lys	Trp	Trp	Gly	Leu	Asn	
			720					725					730			
CTG	CAG	TTC	CTG	CTG	GTT	TTC	CTC	TGC	ACC	TTC	ATG	CAG	ATT	GTC	ATC	2679
Leu	Gln	Phe	Leu	Leu	Val	Phe	Leu	Cys	Thr	Phe	Met	Gln	Ile	Val	Ile	
		735					740					745				
TGT	GTG	ATC	TGG	CTC	TAC	ACC	GCG	CCC	CCC	TCA	AGC	TAC	CGC	AAC	CAG	2727
Cys	Val	Ile	Trp	Leu	Tyr	Thr	Ala	Pro	Pro	Ser	Ser	Tyr	Arg	Asn	Gln	
	750					755					760					
GAG	CTG	GAG	GAT	GAG	ATC	ATC	TTC	ATC	ACG	TGC	CAC	GAG	GGC	TCC	CTC	2775
Glu	Leu	Glu	Asp	Glu	Ile	Ile	Phe	Ile	Thr	Cys	His	Glu	Gly	Ser	Leu	
765					770					775					780	
ATG	GCC	CTG	GGC	TTC	CTG	ATC	GGC	TAC	ACC	TGC	CTG	CTG	GCT	GCC	ATC	2823
Met	Ala	Leu	Gly	Phe	Leu	Ile	Gly	Tyr	Thr	Cys	Leu	Leu	Ala	Ala	Ile	
				785				790						795		
TGC	TTC	TTC	TTT	GCC	TTC	AAG	TCC	CGG	AAG	CTG	CCG	GAG	AAC	TTC	AAT	2871
Cys	Phe	Phe	Phe	Ala	Phe	Lys	Ser	Arg	Lys	Leu	Pro	Glu	Asn	Phe	Asn	
			800					805					810			
GAA	GCC	AAG	TTC	ATC	ACC	TTC	AGC	ATG	CTC	ATC	TTC	TTC	ATC	GTC	TGG	2919
Glu	Ala	Lys	Phe	Ile	Thr	Phe	Ser	Met	Leu	Ile	Phe	Phe	Ile	Val	Trp	
		815					820					825				
ATC	TCC	TTC	ATT	CCA	GCC	TAT	GCC	AGC	ACC	TAT	GGC	AAG	TTT	GTC	TCT	2967
Ile	Ser	Phe	Ile	Pro	Ala	Tyr	Ala	Ser	Thr	Tyr	Gly	Lys	Phe	Val	Ser	
	830					835					840					
GCC	GTA	GAG	GTG	ATT	GCC	ATC	CTG	GCA	GCC	AGC	TTT	GGC	TTG	CTG	GCG	3015
Ala	Val	Glu	Val	Ile	Ala	Ile	Leu	Ala	Ala	Ser	Phe	Gly	Leu	Leu	Ala	
845					850					855					860	
TGC	ATC	TTC	TTC	AAC	AAG	ATC	TAC	ATC	ATT	CTC	TTC	AAG	CCA	TCC	CGC	3063
Cys	Ile	Phe	Phe	Asn	Lys	Ile	Tyr	Ile	Ile	Leu	Phe	Lys	Pro	Ser	Arg	
				865				870						875		
AAC	ACC	ATC	GAG	GAG	GTG	CGT	TGC	AGC	ACC	GCA	GCT	CAC	GCT	TTC	AAG	3111
Asn	Thr	Ile	Glu	Glu	Val	Arg	Cys	Ser	Thr	Ala	Ala	His	Ala	Phe	Lys	
			880					885					890			

GTG	GCT	GCC	CGG	GCC	ACG	CTG	CGC	CGC	AGC	AAC	GTC	TCC	CGC	AAG	CGG	3159
Val	Ala	Ala	Arg	Ala	Thr	Leu	Arg	Arg	Ser	Asn	Val	Ser	Arg	Lys	Arg	
		895					900					905				
TCC	AGC	AGC	CTT	GGA	GGC	TCC	ACG	GGA	TCC	ACC	CCC	TCC	TCC	TCC	ATC	3207
Ser	Ser	Ser	Leu	Gly	Gly	Ser	Thr	Gly	Ser	Thr	Pro	Ser	Ser	Ser	Ile	
	910					915					920					
AGC	AGC	AAG	AGC	AAC	AGC	GAA	GAC	CCA	TTC	CCA	CGG	CCC	GAG	AGG	CAG	3255
Ser	Ser	Lys	Ser	Asn	Ser	Glu	Asp	Pro	Phe	Pro	Arg	Pro	Glu	Arg	Gln	
925					930					935					940	
AAG	CAG	CAG	CAG	CCG	CTG	GCC	CTA	ACC	CAG	CAA	GAG	CAG	CAG	CAG	CAG	3303
Lys	Gln	Gln	Gln	Pro	Leu	Ala	Leu	Thr	Gln	Gln	Glu	Gln	Gln	Gln	Gln	
				945					950						955	
CCC	CTG	ACC	CTC	CCA	CAG	CAG	CAA	CGA	TCT	CAG	CAG	CAG	CCC	AGA	TGC	3351
Pro	Leu	Thr	Leu	Pro	Gln	Gln	Gln	Arg	Ser	Gln	Gln	Gln	Pro	Arg	Cys	
			960					965					970			
AAG	CAG	AAG	GTC	ATC	TTT	GGC	AGC	GGC	ACG	GTC	ACC	TTC	TCA	CTG	AGC	3399
Lys	Gln	Lys	Val	Ile	Phe	Gly	Ser	Gly	Thr	Val	Thr	Phe	Ser	Leu	Ser	
		975					980					985				
TTT	GAT	GAG	CCT	CAG	AAG	AAC	GCC	ATG	GCC	CAC	AGG	AAT	TCT	ACG	CAC	3447
Phe	Asp	Glu	Pro	Gln	Lys	Asn	Ala	Met	Ala	His	Arg	Asn	Ser	Thr	His	
	990					995					1000					
CAG	AAC	TCC	CTG	GAG	GCC	CAG	AAA	AGC	AGC	GAT	ACG	CTG	ACC	CGA	CAC	3495
Gln	Asn	Ser	Leu	Glu	Ala	Gln	Lys	Ser	Ser	Asp	Thr	Leu	Thr	Arg	His	
1005					1010					1015					1020	
CAG	CCA	TTA	CTC	CCG	CTG	CAG	TGC	GGG	GAA	ACG	GAC	TTA	GAT	CTG	ACC	3543
Gln	Pro	Leu	Leu	Pro	Leu	Gln	Cys	Gly	Glu	Thr	Asp	Leu	Asp	Leu	Thr	
			1025					1030						1035		
GTC	CAG	GAA	ACA	GGT	CTG	CAA	GGA	CCT	GTG	GGT	GGA	GAC	CAG	CGG	CCA	3591
Val	Gln	Glu	Thr	Gly	Leu	Gln	Gly	Pro	Val	Gly	Gly	Asp	Gln	Arg	Pro	
			1040					1045					1050			
GAG	GTG	GAG	GAC	CCT	GAA	GAG	TTG	TCC	CCA	GCA	CTT	GTA	GTG	TCC	AGT	3639
Glu	Val	Glu	Asp	Pro	Glu	Glu	Leu	Ser	Pro	Ala	Leu	Val	Val	Ser	Ser	
		1055					1060					1065				
TCA	CAG	AGC	TTT	GTC	ATC	AGT	GGT	GGA	GGC	AGC	ACT	GTT	ACA	GAA	AAC	3687
Ser	Gln	Ser	Phe	Val	Ile	Ser	Gly	Gly	Gly	Ser	Thr	Val	Thr	Glu	Asn	
	1070					1075					1080					
GTA	GTG	AAT	TCA	TAAAATGGAA	GGAGAAGACT	GGGCTAGGGA	GAATGCAGAG									3739
Val	Val	Asn	Ser													
1085																
AGGTTTCTTG	GGGTCCCAGG	GATGAGGAAT	CGCCCCAGAC													

TGACCCATGT TCCCTTTAAA ATTAAAAAAA AGAAGAGCCT TGTGTTTCTG TGGTTGCATT 3919
 TGTCAAAGCA TTGAGATCTC CACGGTCAGA TTTGCTGTTC ACCCACATCT AATGTCTCTT 3979
 CCTCTGTTCT ATCCCACCCA ACAGCTCAGA GATGAAACTA TGGCTTTAAA CTACCCTCCA 4039
 GAGTGTGCAG ACTGATGGGA CATCAAATTT GCCACCACTA GAGCTGAGAG TCTGAAAGAC 4099
 AGAATGTCAC CAGTCCTGCC CAATGCCTTG ACAACAGACT GAATTTTAAA TGTTCACAAC 4159
 ATAAGGAGAA TGTATCTCCT CCTATTTATG AAAACCATAT GATATTTTGT CTCCTACCTG 4219
 CTGCTGCTAT TATGTAACAT CCAGAAGGTT TGCACCCCTC CTATACCATA TGTCTGGTTC 4279
 TGTCCAGGAC ATGATACTGA TGCCATGTTT AGATTCCAGG ATCACAAGAA TCACCTCAAA 4339
 TTGTTAGGAA GGGACTGCAT AAACCAATGA GCTGTATCTG TAATTAATAT TCCTATATGT 4399
 AGCTTTATCC TTAGGAAAAT GCTTCTGTTG TAATAGTCCA TGGACAATAT AAAGTAAAAA 4459
 ATGTCAGTCT GGTATATATA AGGCAGTATT ATTGAGCTCT ATTTCCCCAC CCCACTATCC 4519
 TCACTCCCAT AAGCTAAGCC TTATGTGAGC CCCTTCAGGG ACTCAAGGGT CCAGAAGTCC 4579
 CTCCCATCTC TACCCCAAAG AATTCCTGAA GCCAGATCCA CCCTATCCCT GTACAGAGTA 4639
 AGTTCTCAAT TATTGGCCTG CTAATAGCTG CTAGGGTAGG AAAGCGTGGT TCCAAGAAAG 4699
 ATCCACCCTC AAATGTCGGA GCTATGTTCC CTCCAGCAGT GGTATTAATA CTGCCGGTCA 4759
 CCCAGGCTCT GGAGCCAGAG AGACAGACCG GGGTTCAAGC CATGGCTTCG TCATTTGCAA 4819
 GCTGAGTGAC TGTAGGCAGG GAACCTTAAC CTCTCTAAGC CACAGCTTCT TCATCTTTAA 4879
 AATAAGGATA ATAATCATT CTTCCCCTCA GAGCTCTTAT GTGGATTAAA CGAGATAATG 4939
 TATATAAAGT ACTTTAGCCT GGTACCTAGC ACACAATAAG CATTCAATAA ATATTAGTTA 4999
 ATATTAT 5006

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	3809 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 373..3606
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CAACAGGCAC CTGGCTGCAG CCAGGAAGGA CCGCACGCCC TTTCGCGCAG GAGAGTGGAA 60
 GGAGGGAGCT GTTTGCCAGC ACCGAGGTCT TGCGGCACAG GCAACGCTTG ACCTGAGTCT 120
 TGCAGAATGA AAGGCATCAC AGGAGGCCTC TGCATGATGT GGCTTCCAAA GACTCAAGGA 180
 CCACCCACAT TACAAGTCTG GATTGAGGAA GGCAGAAATG GAGATTCAAA CACCACGTCT 240
 TCTATTATTT TATTAATCAA TCTGTAGACA TGTGTCCCCA CTGCAGGGAG TGAAGTCTC 300
 CAAGGGAGAA ACTTCTGGGA GCCTCCAAAC TCCTAGCTGT CTCATCCCTT GCCCTGGAGA 360
 GACGGCAGAA CC ATG GCA TTT TAT AGC TGC TGC TGG GTC CTC TTG GCA 408
 Met Ala Phe Tyr Ser Cys Cys Trp Val Leu Leu Ala
 1 5 10

CTC ACC TGG CAC ACC TCT GCC TAC GGG CCA GAC CAG CGA GCC CAA AAG 456
 Leu Thr Trp His Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys
 15 20 25

AAG GGG GAC ATT ATC CTT GGG GGG CTC TTT CCT ATT CAT TTT GGA GTA 504
 Lys Gly Asp Ile Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val
 30 35 40

GCA GCT AAA GAT CAA GAT CTC AAA TCA AGG CCG GAG TCT GTG GAA TGT 552
 Ala Ala Lys Asp Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys
 45 50 55 60

ATC AGG TAT AAT TTC CGT GGG TTT CGC TGG TTA CAG GCT ATG ATA TTT 600
 Ile Arg Tyr Asn Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe
 65 70 75

GCC ATA GAG GAG ATA AAC AGC AGC CCA GCC CTT CTT CCC AAC TTG ACG 648
 Ala Ile Glu Glu Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr
 80 85 90

CTG GGA TAC AGG ATA TTT GAC ACT TGC AAC ACC GTT TCT AAG GCC TTG 696
 Leu Gly Tyr Arg Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu
 95 100 105

GAA GCC ACC CTG AGT TTT GTT GCT CAA AAC AAA ATT GAT TCT TTG AAC 744
 Glu Ala Thr Leu Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn
 110 115 120

223 136256

CTT Leu 125	GAT Asp	GAG Glu	TTC Phe	TGC Cys	AAC Asn 130	TGC Cys	TCA Ser	GAG Glu	CAC His	ATT Ile 135	CCC Pro	TCT Ser	ACG Thr	ATT Ile	GCT Ala 140	792
GTG Val	GTG Val	GGA Gly	GCA Ala	ACT Thr 145	GGC Gly	TCA Ser	GGC Gly	GTC Val	TCC Ser 150	ACG Thr	GCA Ala	GTG Val	GCA Ala	AAT Asn 155	CTG Leu	840
CTG Leu	GGG Gly	CTC Leu	TTC Phe 160	TAC Tyr	ATT Ile	CCC Pro	CAG Gln	GTC Val 165	AGT Ser	TAT Tyr	GCC Ala	TCC Ser	TCC Ser	AGC Ser	AGA Arg	888
CTC Leu	CTC Leu	AGC Ser 175	AAC Asn	AAG Lys	AAT Asn	CAA Gln	TTC Phe 180	AAG Lys	TCT Ser	TTC Phe	CTC Leu	CGA Arg 185	ACC Thr	ATC Ile	CCC Pro	936
AAT Asn 190	GAT Asp	GAG Glu	CAC His	CAG Gln	GCC Ala 195	ACT Thr	GCC Ala	ATG Met	GCA Ala	GAC Asp	ATC Ile 200	ATC Ile	GAG Glu	TAT Tyr	TTC Phe	984
CGC Arg 205	TGG Trp	AAC Asn	TGG Trp	GTG Val	GGC Gly 210	ACA Thr	ATT Ile	GCA Ala	GCT Ala	GAT Asp 215	GAC Asp	GAC Asp	TAT Tyr	GGG Gly	CGG Arg 220	1032
CCG Pro	GGG Gly	ATT Ile	GAG Glu	AAA Lys 225	TTC Phe	CGA Arg	GAG Glu	GAA Glu	GCT Ala 230	GAG Glu	GAA Glu	AGG Arg	GAT Asp	ATC Ile 235	TGC Cys	1080
ATC Ile	GAC Asp	TTC Phe	AGT Ser 240	GAA Glu	CTC Leu	ATC Ile	TCC Ser	CAG Gln 245	TAC Tyr	TCT Ser	GAT Asp	GAG Glu	GAA Glu	GAG Glu	ATC Ile	1128
CAG Gln	CAT His	GTG Val 255	GTA Val	GAG Glu	GTG Val	ATT Ile 260	CAA Gln	AAT Asn	TCC Ser	ACG Thr	GCC Ala	AAA Lys 265	GTC Val	ATC Ile	GTG Val	1176
GTT Val 270	TTC Phe	TCC Ser	AGT Ser	GGC Gly	CCA Pro	GAT Asp 275	CTT Leu	GAG Glu	CCC Pro	CTC Leu	ATC Ile 280	AAG Lys	GAG Glu	ATT Ile	GTC Val	1224
CGG Arg 285	CGC Arg	AAT Asn	ATC Ile	ACG Thr	GGC Gly 290	AAG Lys	ATC Ile	TGG Trp	CTG Leu	GCC Ala 295	AGC Ser	GAG Glu	GCC Ala	TGG Trp	GCC Ala 300	1272
AGC Ser	TCC Ser	TCC Ser	CTG Leu	ATC Ile 305	GCC Ala	ATG Met	CCT Pro	CAG Gln	TAC Tyr 310	TTC Phe	CAC His	GTG Val	GTT Val	GGC Gly 315	GGC Gly	1320
ACC Thr	ATT Ile	GGA Gly	TTC Phe 320	GCT Ala	CTG Leu	AAG Lys	GCT Ala 325	GGG Gly	CAG Gln	ATC Ile	CCA Pro	GGC Gly	TTC Phe 330	CGG Arg	GAA Glu	1368
TTC Phe	CTG Leu	AAG Lys 335	AAG Lys	GTC Val	CAT His	CCC Pro	AGG Arg 340	AAG Lys	TCT Ser	GTC Val	CAC His	AAT Asn 345	GGT Gly	TTT Phe	GCC Ala	1416

AAG Lys 350	GAG Glu 350	TTT Phe 350	TGG Trp 350	GAA Glu 350	GAA Glu 355	ACA Thr 355	TTT Phe 355	AAC Asn 355	TGC Cys 355	CAC His 355	CTC Leu 360	CAA Gln 360	GAA Glu 360	GGT Gly 360	GCA Ala 360	1464
AAA Lys 365	GGA Gly 365	CCT Pro 365	TTA Leu 365	CCT Pro 370	GTG Val 370	GAC Asp 370	ACC Thr 370	TTT Phe 375	CTG Leu 375	AGA Arg 375	GGT Gly 375	CAC His 375	GAA Glu 375	GAA Glu 380	AGT Ser 380	1512
GGC Gly 385	GAC Asp 385	AGG Arg 385	TTT Phe 385	AGC Ser 385	AAC Asn 385	AGC Ser 385	TCG Ser 385	ACA Thr 390	GCC Ala 390	TTC Phe 390	CGA Arg 390	CCC Pro 390	CTC Leu 395	TGT Cys 395	ACA Thr 395	1560
GGG Gly 400	GAT Asp 400	GAG Glu 400	AAC Asn 400	ATC Ile 400	AGC Ser 405	AGT Ser 405	GTC Val 405	GAG Glu 405	ACC Thr 405	CCT Pro 410	TAC Tyr 410	ATA Ile 410	GAT Asp 410	TAC Tyr 410	ACG Thr 410	1608
CAT His 415	TTA Leu 415	CGG Arg 415	ATA Ile 415	TCC Ser 420	TAC Tyr 420	AAT Asn 420	GTG Val 420	TAC Tyr 420	TTA Leu 420	GCA Ala 425	GTC Val 425	TAC Tyr 425	TCC Ser 425	ATT Ile 425	GCC Ala 425	1656
CAC His 430	GCC Ala 430	TTG Leu 430	CAA Gln 430	GAT Asp 435	ATA Ile 435	TAT Tyr 435	ACC Thr 435	TGC Cys 435	TTA Leu 435	CCT Pro 440	GGG Gly 440	AGA Arg 440	GGG Gly 440	CTC Leu 440	TTC Phe 440	1704
ACC Thr 445	AAT Asn 445	GGC Gly 445	TCC Ser 445	TGT Cys 450	GCA Ala 450	GAC Asp 450	ATC Ile 450	AAG Lys 455	AAA Lys 455	GTT Val 455	GAG Glu 455	GCG Ala 455	TGG Trp 455	CAG Gln 460	GTC Val 460	1752
CTG Leu 465	AAG Lys 465	CAC His 465	CTA Leu 465	CGG Arg 465	CAT His 465	CTA Leu 465	AAC Asn 470	TTT Phe 470	ACA Thr 470	AAC Asn 470	AAT Asn 470	ATG Met 470	GGG Gly 475	GAG Glu 475	CAG Gln 475	1800
GTG Val 480	ACC Thr 480	TTT Phe 480	GAT Asp 480	GAG Glu 480	TGT Cys 480	GGT Gly 485	GAC Asp 485	CTG Leu 485	GTG Val 485	GGG Gly 485	AAC Asn 485	TAT Tyr 485	TCC Ser 490	ATC Ile 490	ATC Ile 490	1848
AAC Asn 495	TGG Trp 495	CAC His 495	CTC Leu 495	TCC Ser 495	CCA Pro 495	GAG Glu 500	GAT Asp 500	GGC Gly 500	TCC Ser 500	ATC Ile 500	GTG Val 505	TTT Phe 505	AAG Lys 505	GAA Glu 505	GTC Val 505	1896
GGG Gly 510	TAT Tyr 510	TAC Tyr 510	AAC Asn 510	GTC Val 510	TAT Tyr 515	GCC Ala 515	AAG Lys 515	AAG Lys 515	GGA Gly 515	GAA Glu 520	AGA Arg 520	CTC Leu 520	TTC Phe 520	ATC Ile 520	AAC Asn 520	1944
GAG Glu 525	GAG Glu 525	AAA Lys 525	ATC Ile 525	CTG Leu 530	TGG Trp 530	AGT Ser 530	GGG Gly 530	TTC Phe 535	TCC Ser 535	AGG Arg 535	GAG Glu 535	GTG Val 535	CCC Pro 540	TTC Phe 540	TCC Ser 540	1992
AAC Asn 545	TGC Cys 545	AGC Ser 545	CGA Arg 545	GAC Asp 545	TGC Cys 545	CTG Leu 550	GCA Ala 550	GGG Gly 550	ACC Thr 550	AGG Arg 550	AAA Lys 550	GGG Gly 550	ATC Ile 555	ATT Ile 555	GAG Glu 555	2040
GGG Gly 560	GAG Glu 560	CCC Pro 560	ACC Thr 560	TGC Cys 560	TGC Cys 565	TTT Phe 565	GAG Glu 565	TGT Cys 565	GTG Val 565	GAG Glu 570	TGT Cys 570	CCT Pro 570	GAT Asp 570	GGG Gly 570	GAG Glu 570	2088

TAT	AGT	GAT	GAG	ACA	GAT	GCC	AGT	GCC	TGT	AAC	AAG	TGC	CCA	GAT	GAC	2136
Tyr	Ser	Asp	Glu	Thr	Asp	Ala	Ser	Ala	Cys	Asn	Lys	Cys	Pro	Asp	Asp	
	575						580					585				
TTC	TGG	TCC	AAT	GAG	AAC	CAC	ACC	TCC	TGC	ATT	GCC	AAG	GAG	ATC	GAG	2184
Phe	Trp	Ser	Asn	Glu	Asn	His	Thr	Ser	Cys	Ile	Ala	Lys	Glu	Ile	Glu	
	590					595					600					
TTT	CTG	TCG	TGG	ACG	GAG	CCC	TTT	GGG	ATC	GCA	CTC	ACC	CTC	TTT	GCC	2232
Phe	Leu	Ser	Trp	Thr	Glu	Pro	Phe	Gly	Ile	Ala	Leu	Thr	Leu	Phe	Ala	
605					610					615					620	
GTG	CTG	GGC	ATT	TTC	CTG	ACA	GCC	TTT	GTG	CTG	GGT	GTG	TTT	ATC	AAG	2280
Val	Leu	Gly	Ile	Phe	Leu	Thr	Ala	Phe	Val	Leu	Gly	Val	Phe	Ile	Lys	
				625					630					635		
TTC	CGC	AAC	ACA	CCC	ATT	GTC	AAG	GCC	ACC	AAC	CGA	GAG	CTC	TCC	TAC	2328
Phe	Arg	Asn	Thr	Pro	Ile	Val	Lys	Ala	Thr	Asn	Arg	Glu	Leu	Ser	Tyr	
			640					645					650			
CTC	CTC	CTC	TTC	TCC	CTG	CTC	TGC	TGC	TTC	TCC	AGC	TCC	CTG	TTC	TTC	2376
Leu	Leu	Leu	Phe	Ser	Leu	Leu	Cys	Cys	Phe	Ser	Ser	Ser	Leu	Phe	Phe	
			655				660					665				
ATC	GGG	GAG	CCC	CAG	GAC	TGG	ACG	TGC	CGC	CTG	CGC	CAG	CCG	GCC	TTT	2424
Ile	Gly	Glu	Pro	Gln	Asp	Trp	Thr	Cys	Arg	Leu	Arg	Gln	Pro	Ala	Phe	
	670					675					680					
GGC	ATC	AGC	TTC	GTG	CTC	TGC	ATC	TCA	TGC	ATC	CTG	GTG	AAA	ACC	AAC	2472
Gly	Ile	Ser	Phe	Val	Leu	Cys	Ile	Ser	Cys	Ile	Leu	Val	Lys	Thr	Asn	
685					690					695					700	
CGT	GTC	CTC	CTG	GTG	TTT	GAG	GCC	AAG	ATC	CCC	ACC	AGC	TTC	CAC	CGC	2520
Arg	Val	Leu	Leu	Val	Phe	Glu	Ala	Lys	Ile	Pro	Thr	Ser	Phe	His	Arg	
				705					710					715		
AAG	TGG	TGG	GGG	CTC	AAC	CTG	CAG	TTC	CTG	CTG	GTT	TTC	CTC	TGC	ACC	2568
Lys	Trp	Trp	Gly	Leu	Asn	Leu	Gln	Phe	Leu	Leu	Val	Phe	Leu	Cys	Thr	
			720					725					730			
TTC	ATG	CAG	ATT	GTC	ATC	TGT	GTG	ATC	TGG	CTC	TAC	ACC	GCG	CCC	CCC	2616
Phe	Met	Gln	Ile	Val	Ile	Cys	Val	Ile	Trp	Leu	Tyr	Thr	Ala	Pro	Pro	
			735				740					745				
TCA	AGC	TAC	CGC	AAC	CAG	GAG	CTG	GAG	GAT	GAG	ATC	ATC	TTC	ATC	ACG	2664
Ser	Ser	Tyr	Arg	Asn	Gln	Glu	Leu	Glu	Asp	Glu	Ile	Ile	Phe	Ile	Thr	
	750					755					760					
TGC	CAC	GAG	GGC	TCC	CTC	ATG	GCC	CTG	GGC	TTC	CTG	ATC	GGC	TAC	ACC	2712
Cys	His	Glu	Gly	Ser	Leu	Met	Ala	Leu	Gly	Phe	Leu	Ile	Gly	Tyr	Thr	
765					770					775					780	
TGC	CTG	CTG	GCT	GCC	ATC	TGC	TTC	TTC	TTT	GCC	TTC	AAG	TCC	CGG	AAG	2760
Cys	Leu	Leu	Ala	Ala	Ile	Cys	Phe	Phe	Phe	Ala	Phe	Lys	Ser	Arg	Lys	
				785					790					795		

CTG CCG GAG AAC TTC AAT GAA GCC AAG TTC ATC ACC TTC AGC ATG CTC Leu Pro Glu Asn Phe Asn Glu Ala Lys Phe Ile Thr Phe Ser Met Leu	2808
800 805 810	
ATC TTC TTC ATC GTC TGG ATC TCC TTC ATT CCA GCC TAT GCC AGC ACC Ile Phe Phe Ile Val Trp Ile Ser Phe Ile Pro Ala Tyr Ala Ser Thr	2856
815 820 825	
TAT GGC AAG TTT GTC TCT GCC GTA GAG GTG ATT GCC ATC CTG GCA GCC Tyr Gly Lys Phe Val Ser Ala Val Glu Val Ile Ala Ile Leu Ala Ala	2904
830 835 840	
AGC TTT GGC TTG CTG GCG TGC ATC TTC TTC AAC AAG ATC TAC ATC ATT Ser Phe Gly Leu Leu Ala Cys Ile Phe Phe Asn Lys Ile Tyr Ile Ile	2952
845 850 855 860	
CTC TTC AAG CCA TCC CGC AAC ACC ATC GAG GAG GTG CGT TGC AGC ACC Leu Phe Lys Pro Ser Arg Asn Thr Ile Glu Glu Val Arg Cys Ser Thr	3000
865 870 875	
GCA GCT CAC GCT TTC AAG GTG GCT GCC CGG GCC ACG CTG CGC CGC AGC Ala Ala His Ala Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg Ser	3048
880 885 890	
AAC GTC TCC CGC AAG CGG TCC AGC AGC CTT GGA GGC TCC ACG GGA TCC Asn Val Ser Arg Lys Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly Ser	3096
895 900 905	
ACC CCC TCC TCC TCC ATC AGC AGC AAG AGC AAC AGC GAA GAC CCA TTC Thr Pro Ser Ser Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Pro Phe	3144
910 915 920	
CCA CAG CCC GAG AGG CAG AAG CAG CAG CAG CCG CTG GCC CTA ACC CAG Pro Gln Pro Glu Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu Thr Gln	3192
925 930 935 940	
CAA GAG CAG CAG CAG CAG CCC CTG ACC CTC CCA CAG CAG CAA CGA TCT Gln Glu Gln Gln Gln Gln Pro Leu Thr Leu Pro Gln Gln Gln Arg Ser	3240
945 950 955	
CAG CAG CAG CCC AGA TGC AAG CAG AAG GTC ATC TTT GGC AGC GGC ACG Gln Gln Gln Pro Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly Thr	3288
960 965 970	
GTC ACC TTC TCA CTG AGC TTT GAT GAG CCT CAG AAG AAC GCC ATG GCC Val Thr Phe Ser Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met Ala	3336
975 980 985	
CAC GGG AAT TCT ACG CAC CAG AAC TCC CTG GAG GCC CAG AAA AGC AGC His Gly Asn Ser Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser Ser	3384
990 995 1000	
GAT ACG CTG ACC CGA CAC CAG CCA TTA CTC CCG CTG CAG TGC GGG GAA Asp Thr Leu Thr Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly Glu	3432
1005 1010 1015 1020	

ACG GAC TTA GAT CTG ACC GTC CAG GAA ACA GGT CTG CAA GGA CCT GTG 3480
 Thr Asp Leu Asp Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro Val
 1025 1030 1035
 GGT GGA GAC CAG CGG CCA GAG GTG GAG GAC CCT GAA GAG TTG TCC CCA 3528
 Gly Gly Asp Gln Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser Pro
 1040 1045 1050
 GCA CTT GTA GTG TCC AGT TCA CAG AGC TTT GTC ATC AGT GGT GGA GGC 3576
 Ala Leu Val Val Ser Ser Ser Gln Ser Phe Val Ile Ser Gly Gly Gly
 1055 1060 1065
 AGC ACT GTT ACA GAA AAC GTA GTG AAT TCA TAAATGGAA GGAGAAGACT 3626
 Ser Thr Val Thr Glu Asn Val Val Asn Ser
 1070 1075
 GGGCTAGGGA GAATGCAGAG AGGTTTCTTG GGGTCCCAGG GATGAGGAAT CGCCCCAGAC 3686
 TCCTTTCCTC TGAGGAAGAA GGGATAATAG ACACATCAAA TGCCCCGAAT TTAGTCACAC 3746
 CATCTTAAAT GACAGTGAAT TGACCCATGT TCCCTTTAAA AAAAAAAAAA AAAAAGCGGC 3806
 CGC 3809

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 574..3810
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CGGGACTCTC CAGGCCGGCT CAGGCACCGG ACTGTAGGTG TATTTGGAGG GATTTGGAGG 60
 CTGGAGACCC CAGGAAGCAC GCAGGCGGGA GCAGGCAAGG GGCGGAGCCC CGGGCCCGGC 120
 CAAGGTGGCC GTCAGAGGGT/CTGCGGGGAG GCAGTAGCTT GACCCAAGGC GACCAGGGAA 180

CTTCAGACGG	TAGCACGCCA	CTCAAACAAA	TTAACTTGAC	ATCGCAAGCT	GGGCGGGCTG	240
GTACGACATC	CTGACTTCAG	CATCCAGCTG	TTCCTGGGCA	GACAGAGGGC	CAACAGGTGT	300
TCCTGTGGAA	GAAGCCAGGA	CAAGGACTCC	AGAAAACATC	TCGGGCAGCC	TCTACATGAT	360
GTCACCTTCTC	AGGACTCGAG	GACCAGCCAC	CCTACACCTC	TACTACAGAG	AAGGCAGAAA	420
TGGAGACCCA	AAGGCCATCA	CTCCTGCTCT	GTCACTAACC	ACTCTGTAAT	CATGTCTCCC	480
CACCAGAAGG	TGTGAACCGC	ACCAGGGCCG	TGGAGTTCTC	GGGCTCCCAA	TCCACTGACA	540
CCTTTACCTG	TCCCCTGAAG	AGAAGGCAAC	GCT ATG GCA TCG TAC AGC TGC TGT	Met Ala Ser Tyr Ser Cys Cys		594
			1	5		
TTG GCC CTA	TTG GCT CTT	GCC TGG CAC	TCC TCT GCC	TAT GGG CCT	GAC	642
Leu Ala Leu	Leu Ala Leu	Ala Trp His	Ser Ser Ala	Tyr Gly Pro	Asp	
10		15		20		
CAG CGA GCC	CAA AAG AAG	GGG GAC ATT	ATC CTA GGA	GGT CTC TTT	CCT	690
Gln Arg Ala	Gln Lys Lys	Gly Asp Ile	Ile Leu Gly	Gly Leu Phe	Pro	
25		30	35			
ATC CAT TTT	GGA GTA GCA	GCC AAA GAT	CAA GAT CTG	AAG TCA AGA	CCA	738
Ile His Phe	Gly Val Ala	Ala Lys Asp	Gln Asp Leu	Lys Ser Arg	Pro	
40		45	50		55	
GAG TCT GTG	GAG TGC ATT	AGG TAT AAC	TTC CGT GGA	TTC CGA TGG	TTA	786
Glu Ser Val	Glu Cys Ile	Arg Tyr Asn	Phe Arg Gly	Phe Arg Trp	Leu	
	60		65	70		
CAA GCC ATG	ATA TTC GCC	ATA GAG GAG	ATA AAC AGC	AGC CCC TCC	CTT	834
Gln Ala Met	Ile Phe Ala	Ile Glu Glu	Ile Asn Ser	Ser Pro Ser	Leu	
	75		80	85		
CTT CCC AAC	ATG ACA CTG	GGA TAT AGG	ATA TTT GAC	ACC TGT AAC	ACC	882
Leu Pro Asn	Met Thr Leu	Gly Tyr Arg	Ile Phe Asp	Thr Cys Asn	Thr	
	90	95	100			
GTC TCC AAG	GCG CTG GAA	GCC ACC TTG	AGT TTT GTT	GCC CAG AAC	AAA	930
Val Ser Lys	Ala Leu Glu	Ala Thr Leu	Ser Phe Val	Ala Gln Asn	Lys	
105		110	115			
ATC GAT TCT	TTG AAC CTG	GAC GAG TTC	TGC AAC TGC	TCT GAG CAC	ATC	978
Ile Asp Ser	Leu Asn Leu	Asp Glu Phe	Cys Asn Cys	Ser Glu His	Ile	
120		125	130		135	
CCT TCG ACC	ATT GCC GTG	GTG GGA GCC	ACC GGC TCC	GGT GTC TCC	ACG	1026
Pro Ser Thr	Ile Ala Val	Val Gly Ala	Thr Gly Ser	Gly Val Ser	Thr	
	140		145	150		
GCG GTA GCC	AAC CTG CTG	GGA CTT TTC	TAC ATC CCC	CAG GTG AGC	TAC	1074
Ala Val Ala	Asn Leu Leu	Gly Leu Phe	Tyr Ile Pro	Gln Val Ser	Tyr	
	155		160	165		

GCC Ala	TCC Ser	TCC Ser	AGC Ser	AGG Arg	CTC Leu	CTC Leu	AGC Ser	AAT Asn	AAG Lys	AAC Asn	CAG Gln	TAC Tyr	AAA Lys	TCC Ser	TTC Phe	1122
		170					175					180				
CTC Leu	CGC Arg	ACC Thr	ATT Ile	CCC Pro	AAT Asn	GAC Asp	GAA Glu	CAC His	CAG Gln	GCA Ala	ACC Thr	GCG Ala	ATG Met	GCC Ala	GAC Asp	1170
	185					190					195					
ATC Ile	ATC Ile	GAG Glu	TAC Tyr	TTC Phe	CGC Arg	TGG Trp	AAC Asn	TGG Trp	GTG Val	GGC Gly	ACA Thr	ATT Ile	GCA Ala	GCT Ala	GAT Asp	1218
200					205					210					215	
GAC Asp	GAC Asp	TAT Tyr	GGC Gly	AGA Arg	CCT Pro	GGC Gly	ATT Ile	GAG Glu	AAG Lys	TTC Phe	CGA Arg	GAG Glu	GAA Glu	GCC Ala	GAA Glu	1266
				220					225					230		
GAG Glu	AGG Arg	GAT Asp	ATC Ile	TGC Cys	ATT Ile	GAT Asp	TTT Phe	AGC Ser	GAG Glu	CTC Leu	ATC Ile	TCC Ser	CAG Gln	TAC Tyr	TCT Ser	1314
			235					240					245			
GAC Asp	GAG Glu	GAA Glu	GAG Glu	ATC Ile	CAG Gln	CAG Gln	GTG Val	GTC Val	GAA Glu	GTG Val	ATC Ile	CAA Gln	AAC Asn	TCT Ser	ACG Thr	1362
		250					255					260				
GCC Ala	AAG Lys	GTC Val	ATT Ile	GTC Val	GTT Val	TTC Phe	TCC Ser	AGC Ser	GGC Gly	CCG Pro	GAC Asp	CTA Leu	GAA Glu	CCT Pro	CTC Leu	1410
	265					270					275					
ATC Ile	AAG Lys	GAG Glu	ATT Ile	GTG Val	CGG Arg	CGT Arg	AAC Asn	ATC Ile	ACA Thr	GGC Gly	AGG Arg	ATC Ile	TGG Trp	CTG Leu	GCT Ala	1458
280					285					290					295	
AGC Ser	GAG Glu	GCC Ala	TGG Trp	GCC Ala	AGT Ser	TCC Ser	TCG Ser	CTG Leu	ATT Ile	GCT Ala	ATG Met	CCT Pro	GAG Glu	TAT Tyr	TTC Phe	1506
				300					305					310		
CAT His	GTA Val	GTC Val	GGG Gly	GGC Gly	ACC Thr	ATT Ile	GGG Gly	TTC Phe	GGT Gly	CTG Leu	AAG Lys	GCT Ala	GGG Gly	CAG Gln	ATT Ile	1554
			315					320					325			
CCA Pro	GGC Gly	TTC Phe	AGA Arg	GAA Glu	TTC Phe	CTA Leu	CAG Gln	AAA Lys	GTT Val	CAT His	CCT Pro	AGG Arg	AAG Lys	TCT Ser	GTC Val	1602
		330					335					340				
CAC His	AAT Asn	GGT Gly	TTT Phe	GCC Ala	AAA Lys	GAG Glu	TTT Phe	TGG Trp	GAA Glu	GAA Glu	ACT Thr	TTT Phe	AAT Asn	TGC Cys	CAC His	1650
	345					350					355					
CTC Leu	CAA Gln	GAA Glu	GGC Gly	GCA Ala	AAA Lys	GGA Gly	CCT Pro	TTA Leu	CCT Pro	GTG Val	GAC Asp	ACC Thr	TTC Phe	GTG Val	AGA Arg	1698
360					365					370					375	
AGT Ser	CAC His	GAA Glu	GAA Glu	GGT Gly	GGC Gly	AAC Asn	AGG Arg	TTA Leu	CTC Leu	AAT Asn	AGC Ser	TCT Ser	ACT Thr	GCC Ala	TTC Phe	1746
				380					385					390		

CGA	CCC	CTC	TGC	ACA	GGG	GAT	GAG	AAC	ATC	AAC	AGT	GTG	GAG	ACC	CCT	1794
Arg	Pro	Leu	Cys	Thr	Gly	Asp	Glu	Asn	Ile	Asn	Ser	Val	Glu	Thr	Pro	
			395					400					405			
TAC	ATG	GAT	TAC	GAA	CAT	TTA	CGG	ATA	TCC	TAC	AAT	GTG	TAC	TTA	GCC	1842
Tyr	Met	Asp	Tyr	Glu	His	Leu	Arg	Ile	Ser	Tyr	Asn	Val	Tyr	Leu	Ala	
		410					415					420				
GTC	TAC	TCC	ATT	GCG	CAT	GCC	CTA	CAA	GAT	ATA	TAC	ACC	TGC	TTA	CCC	1890
Val	Tyr	Ser	Ile	Ala	His	Ala	Leu	Gln	Asp	Ile	Tyr	Thr	Cys	Leu	Pro	
	425					430					435					
GGA	AGA	GGG	CTT	TTC	ACC	AAC	GGG	TCC	TGT	GCA	GAC	ATC	AAG	AAG	GTT	1938
Gly	Arg	Gly	Leu	Phe	Thr	Asn	Gly	Ser	Cys	Ala	Asp	Ile	Lys	Lys	Val	
440					445					450					455	
GAG	GCC	TGG	CAG	GTC	TTG	AAG	CAC	CTA	CGG	CAC	CTG	AAC	TTC	ACC	AAC	1986
Glu	Ala	Trp	Gln	Val	Leu	Lys	His	Leu	Arg	His	Leu	Asn	Phe	Thr	Asn	
				460					465					470		
AAC	ATG	GGG	GAG	CAG	GTG	ACC	TTC	GAT	GAG	TGT	GGT	GAT	CTG	GTG	GGG	2034
Asn	Met	Gly	Glu	Gln	Val	Thr	Phe	Asp	Glu	Cys	Gly	Asp	Leu	Val	Gly	
			475					480					485			
AAC	TAT	TCT	ATC	ATC	AAC	TGG	CAC	CTC	TCC	CCA	GAG	GAC	GGC	TCC	ATT	2082
Asn	Tyr	Ser	Ile	Ile	Asn	Trp	His	Leu	Ser	Pro	Glu	Asp	Gly	Ser	Ile	
		490					495					500				
GTG	TTC	AAG	GAA	GTT	GGG	TAC	TAC	AAT	GTG	TAT	GCC	AAG	AAG	GGA	GAA	2130
Val	Phe	Lys	Glu	Val	Gly	Tyr	Tyr	Asn	Val	Tyr	Ala	Lys	Lys	Gly	Glu	
	505					510					515					
AGA	CTC	TTC	ATC	AAT	GAG	GAG	AAG	ATC	TTG	TGG	AGT	GGG	TTC	TCC	AGA	2178
Arg	Leu	Phe	Ile	Asn	Glu	Glu	Lys	Ile	Leu	Trp	Ser	Gly	Phe	Ser	Arg	
520					525					530					535	
GAG	GTG	CCT	TTC	TCC	AAT	TGC	AGC	CGG	GAC	TGT	CAG	GCA	GGG	ACC	AGG	2226
Glu	Val	Pro	Phe	Ser	Asn	Cys	Ser	Arg	Asp	Cys	Gln	Ala	Gly	Thr	Arg	
				540					545					550		
AAG	GGG	ATC	ATC	GAG	GGA	GAG	CCC	ACC	TGC	TGC	TTT	GAG	TGT	GTG	GAG	2274
Lys	Gly	Ile	Ile	Glu	Gly	Glu	Pro	Thr	Cys	Cys	Phe	Glu	Cys	Val	Glu	
			555					560					565			
TGT	CCT	GAT	GGA	GAG	TAC	AGT	GGA	GAG	ACA	GAT	GCG	AGT	GCC	TGT	GAC	2322
Cys	Pro	Asp	Gly	Glu	Tyr	Ser	Gly	Glu	Thr	Asp	Ala	Ser	Ala	Cys	Asp	
		570					575					580				
AAG	TGC	CCG	GAT	GAC	TTC	TGG	TCC	AAT	GAG	AAC	CAC	ACT	TCT	TGC	ATT	2370
Lys	Cys	Pro	Asp	Asp	Phe	Trp	Ser	Asn	Glu	Asn	His	Thr	Ser	Cys	Ile	
	585					590					595					
GCC	AAG	GAG	ATT	GAG	TTT	CTG	GCG	TGG	ACC	GAG	CCC	TTT	GGA	ATC	GCT	2418
Ala	Lys	Glu	Ile	Glu	Phe	Leu	Ala	Trp	Thr	Glu	Pro	Phe	Gly	Ile	Ala	
600					605					610					615	

CTC	ACT	CTC	TTT	GCG	GTG	CTG	GGC	ATT	TTC	CTG	ACC	GCC	TTT	GTG	CTG	2466
Leu	Thr	Leu	Phe	Ala	Val	Leu	Gly	Ile	Phe	Leu	Thr	Ala	Phe	Val	Leu	
				620					625					630		
GGT	GTC	TTC	ATC	AAG	TTC	CGA	AAC	ACA	CCT	ATC	GTC	AAG	GCC	ACC	AAC	2514
Gly	Val	Phe	Ile	Lys	Phe	Arg	Asn	Thr	Pro	Ile	Val	Lys	Ala	Thr	Asn	
			635					640					645			
CGA	GAA	CTG	TCC	TAC	CTC	CTG	CTC	TTC	TCC	CTA	CTC	TGC	TGC	TTC	TCC	2562
Arg	Glu	Leu	Ser	Tyr	Leu	Leu	Leu	Phe	Ser	Leu	Leu	Cys	Cys	Phe	Ser	
		650				655						660				
AGC	TCC	TTG	TTC	TTC	ATT	GGG	GAG	CCC	CAG	GAC	TGG	ACG	TGC	CGC	CTG	2610
Ser	Ser	Leu	Phe	Phe	Ile	Gly	Glu	Pro	Gln	Asp	Trp	Thr	Cys	Arg	Leu	
	665					670					675					
CGA	CAG	CCT	GCT	TTC	GGC	ATC	AGC	TTT	GTG	CTC	TGT	ATC	TCG	TGC	ATC	2658
Arg	Gln	Pro	Ala	Phe	Gly	Ile	Ser	Phe	Val	Leu	Cys	Ile	Ser	Cys	Ile	
680					685				690						695	
TTG	GTG	AAG	ACC	AAT	CGC	GTC	CTC	CTG	GTA	TTT	GAA	GCC	AAG	ATA	CCC	2706
Leu	Val	Lys	Thr	Asn	Arg	Val	Leu	Leu	Val	Phe	Glu	Ala	Lys	Ile	Pro	
				700					705					710		
ACC	AGC	TTC	CAC	CGG	AAG	TGG	TGG	GGG	CTC	AAC	CTG	CAG	TTC	CTG	CTG	2754
Thr	Ser	Phe	His	Arg	Lys	Trp	Trp	Gly	Leu	Asn	Leu	Gln	Phe	Leu	Leu	
			715					720					725			
GTT	TTC	CTC	TGC	ACC	TTC	ATG	CAG	ATC	CTC	ATC	TGC	ATC	ATC	TGG	CTC	2802
Val	Phe	Leu	Cys	Thr	Phe	Met	Gln	Ile	Leu	Ile	Cys	Ile	Ile	Trp	Leu	
		730					735					740				
TAC	ACG	GCG	CCC	CCC	TCT	AGC	TAC	CGC	AAC	CAT	GAG	CTG	GAA	GAC	GAA	2850
Tyr	Thr	Ala	Pro	Pro	Ser	Ser	Tyr	Arg	Asn	His	Glu	Leu	Glu	Asp	Glu	
	745					750					755					
ATC	ATC	TTC	ATC	ACG	TGC	CAT	GAG	GGC	TCA	CTC	ATG	GCA	CTT	GGC	TCC	2898
Ile	Ile	Phe	Ile	Thr	Cys	His	Glu	Gly	Ser	Leu	Met	Ala	Leu	Gly	Ser	
760					765				770						775	
CTG	ATC	GGC	TAT	ACC	TGC	CTG	CTG	GCT	GCC	ATC	TGC	TTC	TTC	TTT	GCC	2946
Leu	Ile	Gly	Tyr	Thr	Cys	Leu	Leu	Ala	Ala	Ile	Cys	Phe	Phe	Phe	Ala	
				780					785					790		
TTC	AAG	TCC	AGG	AAG	TTA	CCA	GAG	AAC	TTC	AAC	GAA	GCC	AAG	TTC	ATT	2994
Phe	Lys	Ser	Arg	Lys	Leu	Pro	Glu	Asn	Phe	Asn	Glu	Ala	Lys	Phe	Ile	
			795					800					805			
ACC	TTC	AGC	ATG	CTC	ATC	TTC	TTC	ATC	GTC	TGG	ATC	TCC	TTC	ATT	CCA	3042
Thr	Phe	Ser	Met	Leu	Ile	Phe	Phe	Ile	Val	Trp	Ile	Ser	Phe	Ile	Pro	
		810					815					820				
GCC	TAT	GCC	AGC	ACC	TAC	GGC	AAG	TTT	GTC	TCT	GCC	GTA	GAG	GTG	ATC	3090
Ala	Tyr	Ala	Ser	Thr	Tyr	Gly	Lys	Phe	Val	Ser	Ala	Val	Glu	Val	Ile	
	825					830					835					

GCC Ala 840	ATT Ile	TTG Leu	GCA Ala	GCC Ala	AGC Ser 845	TTT Phe	GGC Gly	TTA Leu	CTA Leu	GCC Ala 850	TGC Cys	ATC Ile	TTC Phe	TTC Phe	AAC Asn 855	3138
AAG Lys	GTC Val	TAC Tyr	ATT Ile	ATC Ile 860	CTC Leu	TTC Phe	AAG Lys	CCT Pro	TCC Ser 865	CGG Arg	AAC Asn	ACC Thr	ATT Ile	GAG Glu 870	GAA Glu	3186
GTC Val	CGC Arg	TCC Ser	AGC Ser 875	ACC Thr	GCA Ala	GCA Ala	CAT His	GCT Ala 880	TTC Phe	AAA Lys	GTA Val	GCA Ala	GCC Ala 885	CGC Arg	GCC Ala	3234
ACT Thr	CTA Leu	CGC Arg 890	CGT Arg	CCC Pro	AAC Asn	ATC Ile	TCC Ser 895	CGG Arg	AAG Lys	CGG Arg	TCC Ser	AGC Ser 900	AGC Ser	CTT Leu	GGA Gly	3282
GGC Gly 905	TCC Ser	ACC Thr	GGC Gly	TCC Ser	ATT Ile	CCC Pro 910	TCC Ser	TCC Ser	TCC Ser	ATC Ile	AGC Ser 915	AGC Ser	AAA Lys	AGC Ser	AAC Asn	3330
AGC Ser 920	GAA Glu	GAC Asp	CGG Arg	TTC Phe	CCG Pro 925	CAG Gln	CCA Pro	GAG Glu	AGG Arg	CAG Gln 930	AAG Lys	CAA Gln	CAG Gln	CAA Gln	CCG Pro 935	3378
CTG Leu	TCC Ser	CTG Leu	ACC Thr	CAG Gln 940	CAA Gln	GAA Glu	CAG Gln	CAG Gln	CAG Gln	CAG Gln 945	CCC Pro	CTG Leu	ACC Thr	CTC Leu 950	CAC His	3426
CCA Pro	CAG Gln	CAA Gln 955	CAG Gln	CAG Gln	CAG Gln	CCA Pro	CAG Gln	CAG Gln 960	CCG Pro	AGA Arg	TGC Cys	AAA Lys	CAG Gln 965	AAG Lys	GTC Val	3474
ATC Ile	TTC Phe	GGC Gly 970	AGT Ser	GGT Gly	ACG Thr	GTC Val	ACC Thr 975	TTC Phe	TCT Ser	CTG Leu	AGT Ser	TTT Phe 980	GAC Asp	GAG Glu	CCT Pro	3522
CAG Gln 985	AAG Lys	AAT Asn	GCC Ala	ATG Met	GCC Ala	CAC His 990	AGG Arg	AAC Asn	TCC Ser	ATG Met	CGT Arg 995	CAG Gln	AAC Asn	TCC Ser	CTG Leu	3570
GAG Glu 1000	GCC Ala	CAG Gln	AGG Arg	AGC Ser	AAC Asn	GAC Asp	ACC Thr	TTG Leu	GGC Gly	AGA Arg 1010	CAC His	CAG Gln	GCC Ala	CTG Leu 1015	CTT Leu	3618
CCC Pro	CTA Leu	CAG Gln	TGT Cys	GCA Ala 1020	GAT Asp	GCG Ala	GAC Asp	TCA Ser	GAA Glu 1025	ATG Met	ACC Thr	ATT Ile	CAG Gln	GAA Glu 1030	ACG Thr	3666
GGC Gly	CTG Leu	CAA Gln 1035	GGG Gly	CCC Pro	ATG Met	GTG Val	GGG Gly	GAC Asp 1040	CAC His	CAG Gln	CCA Pro	GAA Glu 1045	ATG Met	GAA Glu	AGC Ser	3714
TCA Ser	GAT Asp	GAA Glu 1050	ATG Met	TCC Ser	CCA Pro	GCG Ala	CTG Leu 1055	GTC Val	ATG Met	TCC Ser	ACC Thr	TCT Ser 1060	CGG Arg	AGC Ser	TTC Phe	3762

GTC ATT AGT GGT GGA GGT AGC TCT GTG ACG GAA AAC GTA TTA CAC TCC 3810
 Val Ile Ser Gly Gly Gly Ser Ser Val Thr Glu Asn Val Leu His Ser
 1065 1070 1075

TAATGGAGGG AAAGGCTATC CAGTTGAGAG GTTTTTCTTA GAGCCCTGAG CAAAAGGATG 3870
 GGTCTTCCT TTCTTCCCAG GAAGCCAGGG AGAGTAGGTA CGTCAAAGCC TGTACTCAGT 3930
 TGCACTGCTT TGAATGACAG TGAAGTACT GGTGTGCTCT TTAGAGTTAA AAGAAGAGCC 3990
 ATGTTTTGGG GTCGTTTTCC AGAGCTCAGT ATCACACCTG GGTTTGCTGA AGTCTTTTCC 4050
 TCTGCTCTAT CCACCATCAG TTCAGACGAA AGCAAGGCTC TAAGCTACCC ATCTGCTTCC 4110
 CTCAAAAAAA AAAAAAAAAA A 4131

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1085 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Ala Leu Tyr Ser Cys Cys Trp Ile Leu Leu Ala Phe Ser Thr Trp
 1 5 10 15
 Cys Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys Lys Gly Asp
 20 25 30
 Ile Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Val Lys
 35 40 45
 Asp Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr
 50 55 60
 Asn Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu
 65 70 75 80
 Glu Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Met Thr Leu Gly Tyr
 85 90 95

Arg Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr
 100 105 110
 Leu Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu
 115 120 125
 Phe Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly
 130 135 140
 Ala Thr Gly Ser Gly Ile Ser Thr Ala Val Ala Asn Leu Leu Gly Leu
 145 150 155 160
 Phe Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser
 165 170 175
 Asn Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu
 180 185 190
 His Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn
 195 200 205
 Trp Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile
 210 215 220
 Glu Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp Phe
 225 230 235 240
 Ser Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Lys Ile Gln Gln Val
 245 250 255
 Val Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser
 260 265 270
 Ser Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn
 275 280 285
 Ile Thr Gly Arg Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser
 290 295 300
 Leu Ile Ala Met Pro Glu Tyr Phe His Val Val Gly Gly Thr Ile Gly
 305 310 315 320
 Phe Gly Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Gln
 325 330 335
 Lys Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe
 340 345 350
 Trp Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro
 355 360 365
 Leu Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Gly Gly Ala Arg
 370 375 380
 Leu Ser Asn Ser Pro Thr Ala Phe Arg Pro Leu Cys Thr Gly Glu Glu
 385 390 395 400

Asn	Ile	Ser	Ser	Val	Glu	Thr	Pro	Tyr	Met	Asp	Tyr	Thr	His	Leu	Arg
				405					410					415	
Ile	Ser	Tyr	Asn	Val	Tyr	Leu	Ala	Val	Tyr	Ser	Ile	Ala	His	Ala	Leu
			420					425					430		
Gln	Asp	Ile	Tyr	Thr	Cys	Ile	Pro	Gly	Arg	Gly	Leu	Phe	Thr	Asn	Gly
		435					440					445			
Ser	Cys	Ala	Asp	Ile	Lys	Lys	Val	Glu	Ala	Trp	Gln	Val	Leu	Lys	His
	450					455					460				
Leu	Arg	His	Leu	Asn	Phe	Thr	Ser	Asn	Met	Gly	Glu	Gln	Val	Thr	Phe
465					470					475					480
Asp	Glu	Cys	Gly	Asp	Leu	Ala	Gly	Asn	Tyr	Ser	Ile	Ile	Asn	Trp	His
				485					490					495	
Leu	Ser	Pro	Glu	Asp	Gly	Ser	Ile	Val	Phe	Lys	Glu	Val	Gly	Tyr	Tyr
			500					505					510		
Asn	Val	Tyr	Ala	Lys	Lys	Gly	Glu	Arg	Leu	Phe	Ile	Asn	Asp	Glu	Lys
		515					520					525			
Ile	Leu	Trp	Ser	Gly	Phe	Ser	Arg	Glu	Val	Pro	Phe	Ser	Asn	Cys	Ser
530						535					540				
Arg	Asp	Cys	Leu	Ala	Gly	Thr	Arg	Lys	Gly	Ile	Ile	Glu	Gly	Glu	Pro
545					550					555					560
Thr	Cys	Cys	Phe	Glu	Cys	Val	Glu	Cys	Pro	Asp	Gly	Glu	Tyr	Ser	Asp
				565					570					575	
Glu	Thr	Asp	Ala	Ser	Ala	Cys	Asp	Lys	Cys	Pro	Asp	Asp	Phe	Trp	Ser
			580					585					590		
Asn	Glu	Asn	His	Thr	Ser	Cys	Ile	Ala	Lys	Glu	Ile	Glu	Phe	Leu	Ser
		595					600					605			
Trp	Thr	Glu	Pro	Phe	Gly	Ile	Ala	Leu	Thr	Leu	Phe	Ala	Val	Leu	Gly
	610					615					620				
Ile	Phe	Leu	Thr	Ala	Phe	Val	Leu	Gly	Val	Phe	Ile	Lys	Phe	Arg	Asn
625					630					635					640
Thr	Pro	Ile	Val	Lys	Ala	Thr	Asn	Arg	Glu	Leu	Ser	Tyr	Leu	Leu	Leu
				645					650					655	
Phe	Ser	Leu	Leu	Cys	Cys	Phe	Ser	Ser	Ser	Leu	Phe	Phe	Ile	Gly	Glu
			660					665					670		
Pro	Gln	Asp	Trp	Thr	Cys	Arg	Leu	Arg	Gln	Pro	Ala	Phe	Gly	Ile	Ser
		675					680					685			

Phe 690	Val	Leu	Cys	Ile	Ser	Cys 695	Ile	Leu	Val	Lys	Thr 700	Asn	Arg	Val	Leu
Leu 705	Val	Phe	Glu	Ala	Lys 710	Ile	Pro	Thr	Ser	Phe 715	His	Arg	Lys	Trp	Trp 720
Gly	Leu	Asn	Leu	Gln 725	Phe	Leu	Leu	Val	Phe 730	Leu	Cys	Thr	Phe	Met 735	Gln
Ile	Val	Ile	Cys 740	Ala	Ile	Trp	Leu	Asn 745	Thr	Ala	Pro	Pro	Ser 750	Ser	Tyr
Arg	Asn	His 755	Glu	Leu	Glu	Asp	Glu 760	Ile	Ile	Phe	Ile	Thr 765	Cys	His	Glu
Gly	Ser 770	Leu	Met	Ala	Leu	Gly 775	Phe	Leu	Ile	Gly	Tyr 780	Thr	Cys	Leu	Leu
Ala 785	Ala	Ile	Cys	Phe	Phe 790	Phe	Ala	Phe	Lys	Ser 795	Arg	Lys	Leu	Pro	Glu 800
Asn	Phe	Asn	Glu	Ala 805	Lys	Phe	Ile	Thr	Phe 810	Ser	Met	Leu	Ile	Phe 815	Phe
Ile	Val	Trp	Ile 820	Ser	Phe	Ile	Pro	Ala 825	Tyr	Ala	Ser	Thr	Tyr 830	Gly	Lys
Phe	Val	Ser 835	Ala	Val	Glu	Val	Ile 840	Ala	Ile	Leu	Ala	Ala 845	Ser	Phe	Gly
Leu	Leu 850	Ala	Cys	Ile	Phe	Phe 855	Asn	Lys	Val	Tyr	Ile 860	Ile	Leu	Phe	Lys
Pro 865	Ser	Arg	Asn	Thr	Ile 870	Glu	Glu	Val	Arg	Cys 875	Ser	Thr	Ala	Ala	His 880
Ala	Phe	Lys	Val	Ala 885	Ala	Arg	Ala	Thr	Leu 890	Arg	Arg	Ser	Asn	Val 895	Ser
Arg	Gln	Arg	Ser 900	Ser	Ser	Leu	Gly	Gly 905	Ser	Thr	Gly	Ser	Thr 910	Pro	Ser
Ser	Ser	Ile 915	Ser	Ser	Lys	Ser	Asn 920	Ser	Glu	Asp	Pro	Phe 925	Pro	Gln	Gln
Gln 930	Pro	Lys	Arg	Gln	Lys	Gln 935	Pro	Gln	Pro	Leu	Ala 940	Leu	Ser	Pro	His
Asn 945	Ala	Gln	Gln	Pro	Gln 950	Pro	Arg	Pro	Pro	Ser 955	Thr	Pro	Gln	Pro	Gln 960
Pro	Gln	Ser	Gln 965	Gln	Pro	Pro	Arg	Cys	Lys 970	Gln	Lys	Val	Ile	Phe 975	Gly
Ser	Gly	Thr	Val 980	Thr	Phe	Ser	Leu	Ser 985	Phe	Asp	Glu	Pro	Gln 990	Lys	Thr

(2) INFORMATION FOR SEQ ID NO: 6:

(A) LENGTH: 1088 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Ala	Phe	Tyr	Ser	Cys	Cys	Trp	Val	Leu	Leu	Ala	Leu	Thr	Trp	His
1				5					10					15	
Thr	Ser	Ala	Tyr	Gly	Pro	Asp	Gln	Arg	Ala	Gln	Lys	Lys	Gly	Asp	Ile
			20					25					30		
Ile	Leu	Gly	Gly	Leu	Phe	Pro	Ile	His	Phe	Gly	Val	Ala	Ala	Lys	Asp
		35					40					45			
Gln	Asp	Leu	Lys	Ser	Arg	Pro	Glu	Ser	Val	Glu	Cys	Ile	Arg	Tyr	Asn
	50					55					60				
Phe	Arg	Gly	Phe	Arg	Trp	Leu	Gln	Ala	Met	Ile	Phe	Ala	Ile	Glu	Glu
65					70					75					80

Ile	Asn	Ser	Ser	Pro	Ala	Leu	Leu	Pro	Asn	Leu	Thr	Leu	Gly	Tyr	Arg
				85					90					95	
Ile	Phe	Asp	Thr	Cys	Asn	Thr	Val	Ser	Lys	Ala	Leu	Glu	Ala	Thr	Leu
			100					105					110		
Ser	Phe	Val	Ala	Gln	Asn	Lys	Ile	Asp	Ser	Leu	Asn	Leu	Asp	Glu	Phe
		115					120					125			
Cys	Asn	Cys	Ser	Glu	His	Ile	Pro	Ser	Thr	Ile	Ala	Val	Val	Gly	Ala
	130					135					140				
Thr	Gly	Ser	Gly	Val	Ser	Thr	Ala	Val	Ala	Asn	Leu	Leu	Gly	Leu	Phe
145					150					155					160
Tyr	Ile	Pro	Gln	Val	Ser	Tyr	Ala	Ser	Ser	Ser	Arg	Leu	Leu	Ser	Asn
			165					170						175	
Lys	Asn	Gln	Phe	Lys	Ser	Phe	Leu	Arg	Thr	Ile	Pro	Asn	Asp	Glu	His
			180					185					190		
Gln	Ala	Thr	Ala	Met	Ala	Asp	Ile	Ile	Glu	Tyr	Phe	Arg	Trp	Asn	Trp
		195					200					205			
Val	Gly	Thr	Ile	Ala	Ala	Asp	Asp	Asp	Tyr	Gly	Arg	Pro	Gly	Ile	Glu
	210					215					220				
Lys	Phe	Arg	Glu	Glu	Ala	Glu	Glu	Arg	Asp	Ile	Cys	Ile	Asp	Phe	Ser
225					230					235					240
Glu	Leu	Ile	Ser	Gln	Tyr	Ser	Asp	Glu	Glu	Glu	Ile	Gln	His	Val	Val
				245					250					255	
Glu	Val	Ile	Gln	Asn	Ser	Thr	Ala	Lys	Val	Ile	Val	Val	Phe	Ser	Ser
			260					265					270		
Gly	Pro	Asp	Leu	Glu	Pro	Leu	Ile	Lys	Glu	Ile	Val	Arg	Arg	Asn	Ile
		275					280					285			
Thr	Gly	Lys	Ile	Trp	Leu	Ala	Ser	Glu	Ala	Trp	Ala	Ser	Ser	Ser	Leu
	290					295					300				
Ile	Ala	Met	Pro	Gln	Tyr	Phe	His	Val	Val	Gly	Gly	Thr	Ile	Gly	Phe
305					310					315					320
Ala	Leu	Lys	Ala	Gly	Gln	Ile	Pro	Gly	Phe	Arg	Glu	Phe	Leu	Lys	Lys
				325					330					335	
Val	His	Pro	Arg	Lys	Ser	Val	His	Asn	Gly	Phe	Ala	Lys	Glu	Phe	Trp
			340					345					350		
Glu	Glu	Thr	Phe	Asn	Cys	His	Leu	Gln	Glu	Gly	Ala	Lys	Gly	Pro	Leu
		355					360					365			

Pro	Val	Asp	Thr	Phe	Leu	Arg	Gly	His	Glu	Glu	Ser	Gly	Asp	Arg	Phe	370	375	380
Ser	Asn	Ser	Ser	Thr	Ala	Phe	Arg	Pro	Leu	Cys	Thr	Gly	Asp	Glu	Asn	385	390	395
Ile	Ser	Ser	Val	Glu	Thr	Pro	Tyr	Ile	Asp	Tyr	Thr	His	Leu	Arg	Ile	405	410	415
Ser	Tyr	Asn	Val	Tyr	Leu	Ala	Val	Tyr	Ser	Ile	Ala	His	Ala	Leu	Gln	420	425	430
Asp	Ile	Tyr	Thr	Cys	Leu	Pro	Gly	Arg	Gly	Leu	Phe	Thr	Asn	Gly	Ser	435	440	445
Cys	Ala	Asp	Ile	Lys	Lys	Val	Glu	Ala	Trp	Gln	Val	Leu	Lys	His	Leu	450	455	460
Arg	His	Leu	Asn	Phe	Thr	Asn	Asn	Met	Gly	Glu	Gln	Val	Thr	Phe	Asp	465	470	475
Glu	Cys	Gly	Asp	Leu	Val	Gly	Asn	Tyr	Ser	Ile	Ile	Asn	Trp	His	Leu	485	490	495
Ser	Pro	Glu	Asp	Gly	Ser	Ile	Val	Phe	Lys	Glu	Val	Gly	Tyr	Tyr	Asn	500	505	510
Val	Tyr	Ala	Lys	Lys	Gly	Glu	Arg	Leu	Phe	Ile	Asn	Glu	Glu	Lys	Ile	515	520	525
Leu	Trp	Ser	Gly	Phe	Ser	Arg	Glu	Pro	Leu	Thr	Phe	Val	Leu	Ser	Val	530	535	540
Leu	Gln	Val	Pro	Phe	Ser	Asn	Cys	Ser	Arg	Asp	Cys	Leu	Ala	Gly	Thr	545	550	555
Arg	Lys	Gly	Ile	Ile	Glu	Gly	Glu	Pro	Thr	Cys	Cys	Phe	Glu	Cys	Val	565	570	575
Glu	Cys	Pro	Asp	Gly	Glu	Tyr	Ser	Asp	Glu	Thr	Asp	Ala	Ser	Ala	Cys	580	585	590
Asn	Lys	Cys	Pro	Asp	Asp	Phe	Trp	Ser	Asn	Glu	Asn	His	Thr	Ser	Cys	595	600	605
Ile	Ala	Lys	Glu	Ile	Glu	Phe	Leu	Ser	Trp	Thr	Glu	Pro	Phe	Gly	Ile	610	615	620
Ala	Leu	Thr	Leu	Phe	Ala	Val	Leu	Gly	Ile	Phe	Leu	Thr	Ala	Phe	Val	625	630	635
Leu	Gly	Val	Phe	Ile	Lys	Phe	Arg	Asn	Thr	Pro	Ile	Val	Lys	Ala	Thr	645	650	655

Asn	Arg	Glu	Leu	Ser	Tyr	Leu	Leu	Leu	Phe	Ser	Leu	Leu	Cys	Cys	Phe
			660					665					670		
Ser	Ser	Ser	Leu	Phe	Phe	Ile	Gly	Glu	Pro	Gln	Asp	Trp	Thr	Cys	Arg
		675					680					685			
Leu	Arg	Gln	Pro	Ala	Phe	Gly	Ile	Ser	Phe	Val	Leu	Cys	Ile	Ser	Cys
	690					695					700				
Ile	Leu	Val	Lys	Thr	Asn	Arg	Val	Leu	Leu	Val	Phe	Glu	Ala	Lys	Ile
705					710					715					720
Pro	Thr	Ser	Phe	His	Arg	Lys	Trp	Trp	Gly	Leu	Asn	Leu	Gln	Phe	Leu
				725					730					735	
Leu	Val	Phe	Leu	Cys	Thr	Phe	Met	Gln	Ile	Val	Ile	Cys	Val	Ile	Trp
			740					745					750		
Leu	Tyr	Thr	Ala	Pro	Pro	Ser	Ser	Tyr	Arg	Asn	Gln	Glu	Leu	Glu	Asp
		755					760					765			
Glu	Ile	Ile	Phe	Ile	Thr	Cys	His	Glu	Gly	Ser	Leu	Met	Ala	Leu	Gly
	770					775					780				
Phe	Leu	Ile	Gly	Tyr	Thr	Cys	Leu	Leu	Ala	Ala	Ile	Cys	Phe	Phe	Phe
785					790					795					800
Ala	Phe	Lys	Ser	Arg	Lys	Leu	Pro	Glu	Asn	Phe	Asn	Glu	Ala	Lys	Phe
				805					810					815	
Ile	Thr	Phe	Ser	Met	Leu	Ile	Phe	Phe	Ile	Val	Trp	Ile	Ser	Phe	Ile
			820					825					830		
Pro	Ala	Tyr	Ala	Ser	Thr	Tyr	Gly	Lys	Phe	Val	Ser	Ala	Val	Glu	Val
		835					840					845			
Ile	Ala	Ile	Leu	Ala	Ala	Ser	Phe	Gly	Leu	Leu	Ala	Cys	Ile	Phe	Phe
	850					855					860				
Asn	Lys	Ile	Tyr	Ile	Ile	Leu	Phe	Lys	Pro	Ser	Arg	Asn	Thr	Ile	Glu
865					870					875					880
Glu	Val	Arg	Cys	Ser	Thr	Ala	Ala	His	Ala	Phe	Lys	Val	Ala	Ala	Arg
				885					890					895	
Ala	Thr	Leu	Arg	Arg	Ser	Asn	Val	Ser	Arg	Lys	Arg	Ser	Ser	Ser	Leu
			900					905					910		
Gly	Gly	Ser	Thr	Gly	Ser	Thr	Pro	Ser	Ser	Ser	Ile	Ser	Ser	Lys	Ser
		915					920					925			
Asn	Ser	Glu	Asp	Pro	Phe	Pro	Arg	Pro	Glu	Arg	Gln	Lys	Gln	Gln	Gln
	930					935					940				

Pro Leu Ala Leu Thr Gln Gln Glu Gln Gln Gln Gln Pro Leu Thr Leu
 945 950 955 960
 Pro Gln Gln Gln Arg Ser Gln Gln Gln Pro Arg Cys Lys Gln Lys Val
 965 970 975
 Ile Phe Gly Ser Gly Thr Val Thr Phe Ser Leu Ser Phe Asp Glu Pro
 980 985 990
 Gln Lys Asn Ala Met Ala His Arg Asn Ser Thr His Gln Asn Ser Leu
 995 1000 1005
 Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr Arg His Gln Pro Leu Leu
 1010 1015 1020
 Pro Leu Gln Cys Gly Glu Thr Asp Leu Asp Leu Thr Val Gln Glu Thr
 1025 1030 1035 1040
 Gly Leu Gln Gly Pro Val Gly Gly Asp Gln Arg Pro Glu Val Glu Asp
 1045 1050 1055
 Pro Glu Glu Leu Ser Pro Ala Leu Val Val Ser Ser Ser Gln Ser Phe
 1060 1065 1070
 Val Ile Ser Gly Gly Gly Ser Thr Val Thr Glu Asn Val Val Asn Ser
 1075 1080 1085

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1078 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Ala Phe Tyr Ser Cys Cys Trp Val Leu Leu Ala Leu Thr Trp His
 1 5 10 15
 Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys Lys Gly Asp Ile
 20 25 30

Ile	Leu	Gly	Leu	Phe	Pro	Ile	His	Phe	Gly	Val	Ala	Ala	Lys	Asp
	35					40						45		
Gln	Asp	Leu	Lys	Ser	Arg	Pro	Glu	Ser	Val	Glu	Cys	Ile	Arg	Tyr
	50					55					60			Asn
Phe	Arg	Gly	Phe	Arg	Trp	Leu	Gln	Ala	Met	Ile	Phe	Ala	Ile	Glu
	65				70					75				80
Ile	Asn	Ser	Ser	Pro	Ala	Leu	Leu	Pro	Asn	Leu	Thr	Leu	Gly	Tyr
				85					90					95
Ile	Phe	Asp	Thr	Cys	Asn	Thr	Val	Ser	Lys	Ala	Leu	Glu	Ala	Thr
			100					105					110	Leu
Ser	Phe	Val	Ala	Gln	Asn	Lys	Ile	Asp	Ser	Leu	Asn	Leu	Asp	Glu
		115					120					125		Phe
Cys	Asn	Cys	Ser	Glu	His	Ile	Pro	Ser	Thr	Ile	Ala	Val	Val	Gly
	130					135					140			Ala
Thr	Gly	Ser	Gly	Val	Ser	Thr	Ala	Val	Ala	Asn	Leu	Leu	Gly	Leu
	145				150					155				160
Tyr	Ile	Pro	Gln	Val	Ser	Tyr	Ala	Ser	Ser	Ser	Arg	Leu	Leu	Ser
				165					170					175
Lys	Asn	Gln	Phe	Lys	Ser	Phe	Leu	Arg	Thr	Ile	Pro	Asn	Asp	Glu
			180					185					190	His
Gln	Ala	Thr	Ala	Met	Ala	Asp	Ile	Ile	Glu	Tyr	Phe	Arg	Trp	Asn
		195					200					205		Trp
Val	Gly	Thr	Ile	Ala	Ala	Asp	Asp	Asp	Tyr	Gly	Arg	Pro	Gly	Ile
	210					215					220			Glu
Lys	Phe	Arg	Glu	Glu	Ala	Glu	Glu	Arg	Asp	Ile	Cys	Ile	Asp	Phe
	225				230					235				240
Glu	Leu	Ile	Ser	Gln	Tyr	Ser	Asp	Glu	Glu	Glu	Ile	Gln	His	Val
				245					250					255
Glu	Val	Ile	Gln	Asn	Ser	Thr	Ala	Lys	Val	Ile	Val	Val	Phe	Ser
			260					265					270	Ser
Gly	Pro	Asp	Leu	Glu	Pro	Leu	Ile	Lys	Glu	Ile	Val	Arg	Arg	Asn
		275					280					285		Ile
Thr	Gly	Lys	Ile	Trp	Leu	Ala	Ser	Glu	Ala	Trp	Ala	Ser	Ser	Ser
	290					295					300			Leu
Ile	Ala	Met	Pro	Gln	Tyr	Phe	His	Val	Val	Gly	Gly	Thr	Ile	Gly
	305				310					315				320
Ala	Leu	Lys	Ala	Gly	Gln	Ile	Pro	Gly	Phe	Arg	Glu	Phe	Leu	Lys
				325					330					335

Val	His	Pro	Arg	Lys	Ser	Val	His	Asn	Gly	Phe	Ala	Lys	Glu	Phe	Trp
			340					345					350		
Glu	Glu	Thr	Phe	Asn	Cys	His	Leu	Gln	Glu	Gly	Ala	Lys	Gly	Pro	Leu
		355					360					365			
Pro	Val	Asp	Thr	Phe	Leu	Arg	Gly	His	Glu	Glu	Ser	Gly	Asp	Arg	Phe
	370					375					380				
Ser	Asn	Ser	Ser	Thr	Ala	Phe	Arg	Pro	Leu	Cys	Thr	Gly	Asp	Glu	Asn
385					390					395					400
Ile	Ser	Ser	Val	Glu	Thr	Pro	Tyr	Ile	Asp	Tyr	Thr	His	Leu	Arg	Ile
				405					410					415	
Ser	Tyr	Asn	Val	Tyr	Leu	Ala	Val	Tyr	Ser	Ile	Ala	His	Ala	Leu	Gln
			420					425					430		
Asp	Ile	Tyr	Thr	Cys	Leu	Pro	Gly	Arg	Gly	Leu	Phe	Thr	Asn	Gly	Ser
		435					440					445			
Cys	Ala	Asp	Ile	Lys	Lys	Val	Glu	Ala	Trp	Gln	Val	Leu	Lys	His	Leu
	450					455					460				
Arg	His	Leu	Asn	Phe	Thr	Asn	Asn	Met	Gly	Glu	Gln	Val	Thr	Phe	Asp
465					470					475					480
Glu	Cys	Gly	Asp	Leu	Val	Gly	Asn	Tyr	Ser	Ile	Ile	Asn	Trp	His	Leu
				485					490					495	
Ser	Pro	Glu	Asp	Gly	Ser	Ile	Val	Phe	Lys	Glu	Val	Gly	Tyr	Tyr	Asn
			500					505					510		
Val	Tyr	Ala	Lys	Lys	Gly	Glu	Arg	Leu	Phe	Ile	Asn	Glu	Glu	Lys	Ile
		515					520					525			
Leu	Trp	Ser	Gly	Phe	Ser	Arg	Glu	Val	Pro	Phe	Ser	Asn	Cys	Ser	Arg
	530					535					540				
Asp	Cys	Leu	Ala	Gly	Thr	Arg	Lys	Gly	Ile	Ile	Glu	Gly	Glu	Pro	Thr
545					550					555					560
Cys	Cys	Phe	Glu	Cys	Val	Glu	Cys	Pro	Asp	Gly	Glu	Tyr	Ser	Asp	Glu
				565					570					575	
Thr	Asp	Ala	Ser	Ala	Cys	Asn	Lys	Cys	Pro	Asp	Asp	Phe	Trp	Ser	Asn
			580					585					590		
Glu	Asn	His	Thr	Ser	Cys	Ile	Ala	Lys	Glu	Ile	Glu	Phe	Leu	Ser	Trp
		595					600					605			
Thr	Glu	Pro	Phe	Gly	Ile	Ala	Leu	Thr	Leu	Phe	Ala	Val	Leu	Gly	Ile
	610					615					620				

Phe 625	Leu	Thr	Ala	Phe	Val 630	Leu	Gly	Val	Phe	Ile 635	Lys	Phe	Arg	Asn	Thr 640
Pro	Ile	Val	Lys	Ala 645	Thr	Asn	Arg	Glu	Leu 650	Ser	Tyr	Leu	Leu	Leu	Phe 655
Ser	Leu	Leu	Cys 660	Cys	Phe	Ser	Ser	Ser	Leu 665	Phe	Phe	Ile	Gly	Glu	Pro 670
Gln	Asp	Trp 675	Thr	Cys	Arg	Leu	Arg 680	Gln	Pro	Ala	Phe	Gly 685	Ile	Ser	Phe 690
Val 690	Leu	Cys	Ile	Ser	Cys	Ile 695	Leu	Val	Lys	Thr 700	Asn	Arg	Val	Leu	Leu 705
Val 705	Phe	Glu	Ala	Lys	Ile 710	Pro	Thr	Ser	Phe	His 715	Arg	Lys	Trp	Trp	Gly 720
Leu	Asn	Leu	Gln	Phe 725	Leu	Leu	Val	Phe	Leu 730	Cys	Thr	Phe	Met	Gln	Ile 735
Val	Ile	Cys	Val 740	Ile	Trp	Leu	Tyr	Thr 745	Ala	Pro	Pro	Ser	Ser 750	Tyr	Arg 755
Asn	Gln	Glu 755	Leu	Glu	Asp	Glu 760	Ile	Ile	Phe	Ile	Thr	Cys 765	His	Glu	Gly 770
Ser 770	Leu	Met	Ala	Leu	Gly	Phe 775	Leu	Ile	Gly	Tyr	Thr 780	Cys	Leu	Leu	Ala 785
Ala 785	Ile	Cys	Phe	Phe	Phe 790	Ala	Phe	Lys	Ser	Arg 795	Lys	Leu	Pro	Glu	Asn 800
Phe	Asn	Glu	Ala	Lys 805	Phe	Ile	Thr	Phe	Ser 810	Met	Leu	Ile	Phe	Phe	Ile 815
Val	Trp	Ile	Ser 820	Phe	Ile	Pro	Ala	Tyr 825	Ala	Ser	Thr	Tyr	Gly 830	Lys	Phe 835
Val	Ser	Ala 835	Val	Glu	Val	Ile	Ala 840	Ile	Leu	Ala	Ala	Ser 845	Phe	Gly	Leu 850
Leu 850	Ala	Cys	Ile	Phe	Phe	Asn 855	Lys	Ile	Tyr	Ile	Ile	Leu	Phe	Lys	Pro 860
Ser 865	Arg	Asn	Thr	Ile	Glu 870	Glu	Val	Arg	Cys	Ser 875	Thr	Ala	Ala	His	Ala 880
Phe	Lys	Val	Ala	Ala 885	Arg	Ala	Thr	Leu	Arg 890	Arg	Ser	Asn	Val	Ser	Arg 895
Lys	Arg	Ser	Ser 900	Ser	Leu	Gly	Gly	Ser 905	Thr	Gly	Ser	Thr	Pro 910	Ser	Ser 915
Ser	Ile	Ser	Ser	Lys	Ser	Asn	Ser	Glu	Asp	Pro	Phe	Pro 925	Gln	Pro	Glu 930

Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu Thr Gln Gln Glu Gln Gln
 930 935 940
 Gln Gln Pro Leu Thr Leu Pro Gln Gln Gln Arg Ser Gln Gln Gln Pro
 945 950 955 960
 Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly Thr Val Thr Phe Ser
 965 970 975
 Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met Ala His Gly Asn Ser
 980 985 990
 Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr
 995 1000 1005
 Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp Leu Asp
 1010 1015 1020
 Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro Val Gly Gly Asp Gln
 1025 1030 1035 1040
 Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser Pro Ala Leu Val Val
 1045 1050 1055
 Ser Ser Ser Gln Ser Phe Val Ile Ser Gly Gly Gly Ser Thr Val Thr
 1060 1065 1070
 Glu Asn Val Val Asn Ser
 1075

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1079 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Ala Ser Tyr Ser Cys Cys Leu Ala Leu Leu Ala Leu Ala Trp His
 1 5 10 15

Ser	Ser	Ala	Tyr	Gly	Pro	Asp	Gln	Arg	Ala	Gln	Lys	Lys	Gly	Asp	Ile
			20						25				30		
Ile	Leu	Gly	Gly	Leu	Phe	Pro	Ile	His	Phe	Gly	Val	Ala	Ala	Lys	Asp
		35					40					45			
Gln	Asp	Leu	Lys	Ser	Arg	Pro	Glu	Ser	Val	Glu	Cys	Ile	Arg	Tyr	Asn
	50					55					60				
Phe	Arg	Gly	Phe	Arg	Trp	Leu	Gln	Ala	Met	Ile	Phe	Ala	Ile	Glu	Glu
65					70					75					80
Ile	Asn	Ser	Ser	Pro	Ser	Leu	Leu	Pro	Asn	Met	Thr	Leu	Gly	Tyr	Arg
				85					90					95	
Ile	Phe	Asp	Thr	Cys	Asn	Thr	Val	Ser	Lys	Ala	Leu	Glu	Ala	Thr	Leu
			100					105					110		
Ser	Phe	Val	Ala	Gln	Asn	Lys	Ile	Asp	Ser	Leu	Asn	Leu	Asp	Glu	Phe
		115					120					125			
Cys	Asn	Cys	Ser	Glu	His	Ile	Pro	Ser	Thr	Ile	Ala	Val	Val	Gly	Ala
	130					135					140				
Thr	Gly	Ser	Gly	Val	Ser	Thr	Ala	Val	Ala	Asn	Leu	Leu	Gly	Leu	Phe
145					150					155					160
Tyr	Ile	Pro	Gln	Val	Ser	Tyr	Ala	Ser	Ser	Ser	Arg	Leu	Leu	Ser	Asn
				165					170					175	
Lys	Asn	Gln	Tyr	Lys	Ser	Phe	Leu	Arg	Thr	Ile	Pro	Asn	Asp	Glu	His
			180					185					190		
Gln	Ala	Thr	Ala	Met	Ala	Asp	Ile	Ile	Glu	Tyr	Phe	Arg	Trp	Asn	Trp
		195					200					205			
Val	Gly	Thr	Ile	Ala	Ala	Asp	Asp	Asp	Tyr	Gly	Arg	Pro	Gly	Ile	Glu
	210					215					220				
Lys	Phe	Arg	Glu	Glu	Ala	Glu	Glu	Arg	Asp	Ile	Cys	Ile	Asp	Phe	Ser
225					230					235					240
Glu	Leu	Ile	Ser	Gln	Tyr	Ser	Asp	Glu	Glu	Glu	Ile	Gln	Gln	Val	Val
				245					250					255	
Glu	Val	Ile	Gln	Asn	Ser	Thr	Ala	Lys	Val	Ile	Val	Val	Phe	Ser	Ser
			260					265					270		
Gly	Pro	Asp	Leu	Glu	Pro	Leu	Ile	Lys	Glu	Ile	Val	Arg	Arg	Asn	Ile
		275					280					285			
Thr	Gly	Arg	Ile	Trp	Leu	Ala	Ser	Glu	Ala	Trp	Ala	Ser	Ser	Ser	Leu
	290					295					300				

Ile	Ala	Met	Pro	Glu	Tyr	Phe	His	Val	Val	Gly	Gly	Thr	Ile	Gly	Phe
305					310					315					320
Gly	Leu	Lys	Ala	Gly	Gln	Ile	Pro	Gly	Phe	Arg	Glu	Phe	Leu	Gln	Lys
				325					330					335	
Val	His	Pro	Arg	Lys	Ser	Val	His	Asn	Gly	Phe	Ala	Lys	Glu	Phe	Trp
			340					345					350		
Glu	Glu	Thr	Phe	Asn	Cys	His	Leu	Gln	Glu	Gly	Ala	Lys	Gly	Pro	Leu
		355					360					365			
Pro	Val	Asp	Thr	Phe	Val	Arg	Ser	His	Glu	Glu	Gly	Gly	Asn	Arg	Leu
	370					375					380				
Leu	Asn	Ser	Ser	Thr	Ala	Phe	Arg	Pro	Leu	Cys	Thr	Gly	Asp	Glu	Asn
385					390					395					400
Ile	Asn	Ser	Val	Glu	Thr	Pro	Tyr	Met	Asp	Tyr	Glu	His	Leu	Arg	Ile
				405					410					415	
Ser	Tyr	Asn	Val	Tyr	Leu	Ala	Val	Tyr	Ser	Ile	Ala	His	Ala	Leu	Gln
			420					425					430		
Asp	Ile	Tyr	Thr	Cys	Leu	Pro	Gly	Arg	Gly	Leu	Phe	Thr	Asn	Gly	Ser
		435					440					445			
Cys	Ala	Asp	Ile	Lys	Lys	Val	Glu	Ala	Trp	Gln	Val	Leu	Lys	His	Leu
	450					455					460				
Arg	His	Leu	Asn	Phe	Thr	Asn	Asn	Met	Gly	Glu	Gln	Val	Thr	Phe	Asp
465					470					475					480
Glu	Cys	Gly	Asp	Leu	Val	Gly	Asn	Tyr	Ser	Ile	Ile	Asn	Trp	His	Leu
				485					490					495	
Ser	Pro	Glu	Asp	Gly	Ser	Ile	Val	Phe	Lys	Glu	Val	Gly	Tyr	Tyr	Asn
			500					505					510		
Val	Tyr	Ala	Lys	Lys	Gly	Glu	Arg	Leu	Phe	Ile	Asn	Glu	Glu	Lys	Ile
		515					520					525			
Leu	Trp	Ser	Gly	Phe	Ser	Arg	Glu	Val	Pro	Phe	Ser	Asn	Cys	Ser	Arg
	530					535					540				
Asp	Cys	Gln	Ala	Gly	Thr	Arg	Lys	Gly	Ile	Ile	Glu	Gly	Glu	Pro	Thr
545					550					555					560
Cys	Cys	Phe	Glu	Cys	Val	Glu	Cys	Pro	Asp	Gly	Glu	Tyr	Ser	Gly	Glu
				565					570					575	
Thr	Asp	Ala	Ser	Ala	Cys	Asp	Lys	Cys	Pro	Asp	Asp	Phe	Trp	Ser	Asn
			580					585					590		

Glu	Asn	His	Thr	Ser	Cys	Ile	Ala	Lys	Glu	Ile	Glu	Phe	Leu	Ala	Trp
		595						600					605		
Thr	Glu	Pro	Phe	Gly	Ile	Ala	Leu	Thr	Leu	Phe	Ala	Val	Leu	Gly	Ile
	610					615					620				
Phe	Leu	Thr	Ala	Phe	Val	Leu	Gly	Val	Phe	Ile	Lys	Phe	Arg	Asn	Thr
625					630					635					640
Pro	Ile	Val	Lys	Ala	Thr	Asn	Arg	Glu	Leu	Ser	Tyr	Leu	Leu	Leu	Phe
				645					650					655	
Ser	Leu	Leu	Cys	Cys	Phe	Ser	Ser	Ser	Leu	Phe	Phe	Ile	Gly	Glu	Pro
			660					665					670		
Gln	Asp	Trp	Thr	Cys	Arg	Leu	Arg	Gln	Pro	Ala	Phe	Gly	Ile	Ser	Phe
		675					680					685			
Val	Leu	Cys	Ile	Ser	Cys	Ile	Leu	Val	Lys	Thr	Asn	Arg	Val	Leu	Leu
	690					695					700				
Val	Phe	Glu	Ala	Lys	Ile	Pro	Thr	Ser	Phe	His	Arg	Lys	Trp	Trp	Gly
705					710					715					720
Leu	Asn	Leu	Gln	Phe	Leu	Leu	Val	Phe	Leu	Cys	Thr	Phe	Met	Gln	Ile
				725					730					735	
Leu	Ile	Cys	Ile	Ile	Trp	Leu	Tyr	Thr	Ala	Pro	Pro	Ser	Ser	Tyr	Arg
			740					745					750		
Asn	His	Glu	Leu	Glu	Asp	Glu	Ile	Ile	Phe	Ile	Thr	Cys	His	Glu	Gly
		755					760					765			
Ser	Leu	Met	Ala	Leu	Gly	Ser	Leu	Ile	Gly	Tyr	Thr	Cys	Leu	Leu	Ala
	770					775					780				
Ala	Ile	Cys	Phe	Phe	Phe	Ala	Phe	Lys	Ser	Arg	Lys	Leu	Pro	Glu	Asn
785					790					795					800
Phe	Asn	Glu	Ala	Lys	Phe	Ile	Thr	Phe	Ser	Met	Leu	Ile	Phe	Phe	Ile
				805					810					815	
Val	Trp	Ile	Ser	Phe	Ile	Pro	Ala	Tyr	Ala	Ser	Thr	Tyr	Gly	Lys	Phe
			820					825					830		
Val	Ser	Ala	Val	Glu	Val	Ile	Ala	Ile	Leu	Ala	Ala	Ser	Phe	Gly	Leu
		835					840					845			
Leu	Ala	Cys	Ile	Phe	Phe	Asn	Lys	Val	Tyr	Ile	Ile	Leu	Phe	Lys	Pro
	850					855					860				
Ser	Arg	Asn	Thr	Ile	Glu	Glu	Val	Arg	Ser	Ser	Thr	Ala	Ala	His	Ala
865					870					875					880
Phe	Lys	Val	Ala	Ala	Arg	Ala	Thr	Leu	Arg	Arg	Pro	Asn	Ile	Ser	Arg
				885						890				895	

Lys Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly Ser Ile Pro Ser Ser
 900 905 910
 Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Arg Phe Pro Gln Pro Glu
 915 920 925
 Arg Gln Lys Gln Gln Gln Pro Leu Ser Leu Thr Gln Gln Glu Gln Gln
 930 935 940
 Gln Gln Pro Leu Thr Leu His Pro Gln Gln Gln Gln Gln Pro Gln Gln
 945 950 955 960
 Pro Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly Thr Val Thr Phe
 965 970 975
 Ser Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met Ala His Arg Asn
 980 985 990
 Ser Met Arg Gln Asn Ser Leu Glu Ala Gln Arg Ser Asn Asp Thr Leu
 995 1000 1005
 Gly Arg His Gln Ala Leu Leu Pro Leu Gln Cys Ala Asp Ala Asp Ser
 1010 1015 1020
 Glu Met Thr Ile Gln Glu Thr Gly Leu Gln Gly Pro Met Val Gly Asp
 1025 1030 1035 1040
 His Gln Pro Glu Met Glu Ser Ser Asp Glu Met Ser Pro Ala Leu Val
 1045 1050 1055
 Met Ser Thr Ser Arg Ser Phe Val Ile Ser Gly Gly Gly Ser Ser Val
 1060 1065 1070
 Thr Glu Asn Val Leu His Ser
 1075

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	15 amino acids
(B) TYPE:	amino acids
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(ii) MOLECULE TYPE:	peptide
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Tyr Lys Asp Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys
1 5 10 15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
(B) TYPE: amino acids
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu Lys Phe Arg Glu Glu
1 5 10 15
Ala Glu Glu Arg Asp Ile Cys
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids
(B) TYPE: amino acids
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Cys Ile Asp Phe Ser Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Lys
1 5 10 15
Ile Gln Gln

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids
(B) TYPE: amino acids
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr His Asn Gly Phe Ala Lys Glu Phe Trp Glu Glu Thr Phe Asn Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids
(B) TYPE: amino acids
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Gly Glu Tyr Ser Asp Glu Thr Asp Ala Ser Ala Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	15 amino acids
(B) TYPE:	amino acids
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn	Thr	Pro	Ile	Val	Lys	Ala	Thr	Asn	Arg	Glu	Leu	Ser	Tyr	Cys
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	15 amino acids
(B) TYPE:	amino acids
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Tyr	Arg	Asn	His	Glu	Leu	Glu	Asp	Glu	Ile	Ile	Phe	Ile	Thr	Cys
1				5					10					15

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala Lys Tyr Cys
1 5 10

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: nucleic acid

(A) NAME/KEY: Modified Base
(B) LOCATION: 13...13
(C) OTHER INFORMATION: Inosine

CCTGCTCGAG ACNARYCGGG ARCTYTSCTA YMT

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	31 base pairs
(B) TYPE:	nucleic
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(ii) MOLECULE TYPE: nucleic acid

(iii) FEATURE:

(A) NAME/KEY:	Modified Base
(B) LOCATION:	13...13
(C) OTHER INFORMATION:	Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGGAATTCCG TTNCGGGWYT TGAASGCRWA S

31

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	32 base pairs
(B) TYPE:	nucleic
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(ii) MOLECULE TYPE: nucleic acid

(iii) FEATURE:

(A) NAME/KEY:	Modified Base
(B) LOCATION:	24...24
(C) OTHER INFORMATION:	Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCTGCTCGAG TCAAGGCTAC GRRNMGNAR YT

32

CGGAATTCCG TTNCGGGWYT TGAASGCRWA S

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	34 base pairs
(B) TYPE:	nucleic
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(ii) MOLECULE TYPE: nucleic acid

(iii) FEATURE:

(A) NAME/KEY:	Modified Base
(B) LOCATION:	26...26
(C) OTHER INFORMATION:	Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGGAATTCCA TTTGGCTTCG TTGAANKTNK CNGG

34

CGGAATTCCA TTTGGCTTCG TTGAANKTNK CNGG